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SARS coronavirus TW HP1

SARS coronavirus TW HP1

Viruses; SRNA positive-strand viruses, no DNA stage; Nidovirales;

Coronaviridae; Coronavirus.

1 (bases 1 to 626)

Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J.,

Mang, J.-Y., Chen, H.-Y. and Chen, Y.-M. Arthur.

Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS

Dupublished
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any Y.-C. Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J.,
Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M.Arthur.
Direct Submission
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                         SARS coronavirus TW-HP1 isolate TW-HP1_SC18 replicase 1B gene, AY451928
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Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J., Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M.Arthur.
Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS
Upublished
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Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J., Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M.Arthur.
Direct Submission
Submitted (28-OCT-2003) National Yang-Ming University, AIDS
Prevention and Research Center, 155, Li-Nong St., Sec.2, Peitou, Taipei, Taiwan 112, R.O.C.
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SARS coronavirus TW-HP4
SARS coronavirus TW-HP4
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.

L bases 1 to 626
Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J.,
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Molecular Epidemiology of SARS in Taiwan - Development of a Simple
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any:-C. Chen,Y.-J., Lee,C.-M., Liu,T.-T., Lu,J.-J., Chan,Y.-J.,
Yang,J.-Y., Chen,H.-Y. and Chen,Y.-M.Arthur.
Direct Submission
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Li Chases, 1 to 6.2.

Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J., Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M. Arthur.

Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS

Unpublished

Dases 1 to 6.26)
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SARS coronavirus TW-HP3
Viruses; sRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
1 (bases 1 to 626)
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Direct Submission
Submitted (28-OCT-2003) National Yang-Ming University, AIDS
Prevention and Research Center, 155, Li-Nong St., Sec.2, Peitou, Taipei, Taiwan 112, R.O.C.
Location/Qualifiers
                                                                            Gaps
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100.0%; Score 25; DB 14; Length 626;
Best Local Similarity 100.0%; Pred. No. 0.53;
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hea 0; Indels
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/db_xref="taxon:264372"
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/isolate="TW-HP2_SC18"
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/codon start=1
/producft="replicase 1B"
/producft="replicase 1B"
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/db_xref="d1:42741339"
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GVITHDVSSAINRPGTGVYREFLTRNPAMRKAVF1SPYNSQNAVASKILGLFTQTYDS
SQGSEYDYVIFTQTTETAHSCNVNRFNVAITRAKIGILCIMSDRDLYD"
                                                                                        Viruses; seRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.

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Nolecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS

C (bases I to 626)
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Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronavirudae; Coronavirus.

1 (bases 1 to 626)
Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J.,
Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M.Arthur.
Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS
Unpublished

2 (bases 1 to 626)
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Direct Submission

Submitted (28-0CT-2003) National Yang-Ming University, AIDS

Prevention and Research Center, 155, Li-Nong St., Sec.2, Peitou, Taipei, Taiwan 112, R.O.C.

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                      Submitted (28-OCT-2003) National Yang-Ming University, AIDS Prevention and Research Center, 155, Li-Nong St., Sec.2, Peitou, Taipei, Taiman 112, R.O.C. Location/Qualifiers
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SARS coronavirus TW-KC3 isolate TW-KC3_SC18 replicase 1B gene,
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    organism="SARS coronavirus TW-KC3"

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/db_xref="G1:42741335"
/translation="ISMATNYDLSVVNARLERKHYVYIGDPAQLPAFRILLTKGTLEP
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SQGSEYDYVIFTQTTETAHSCNVNRFNVAITRAKIGILCIMSDRDLYD"
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SQGSEYDYVIFTQTTETAHSCNVNRFNVAITRAKIGILCIMSDRDLYD"
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Yang,J.-Y., Chen,H.-Y. and Chen,Y.-M.Arthur.

Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS

Unpublished
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SARS coronavirus TW-JC2
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
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/mol type="genomic RNA"
/isolate="TW-JC2_SC18"
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ilarity 100.0%;
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FEATURES

REFERENCE AUTHORS

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ACCESSION VERSION KEYWORDS SOURCE

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Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M.Arthur.

Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS

Lupublished

E 2 (Dasse 1 to 626)

S Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J., Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M.Arthur.

Direct Submission

Submitted (28-OCT-2003) National Yang-Ming University, AIDS Prevention and Research Center, 155, Li-Nong St., Sec.2, Peitou, Taipel, Taiwan 112, R.O.C.

Location/Qualifiers
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GVITHDVSSAINREQUIGVVREFLTRNPAMRKAVFISFYNSONAVASKILGLFTQTVDS
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SARS coronavirus TW-GD1
SARS coronavirus TW-GD1
SARNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 0.53;
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                                                                   codon_start=1
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EYFNSYCRLMKTIGPDMFLGTCRRCPAEIVDTVSALVYDNKLKAHKDKSAQCFKMFYK
GVITHDVSSAINRPQIGVVREFLTRNPAWRKAVFISPYNSQNAVASKILGLPTGTVDS
SQGSEYDYVIFTQTTETAHSCNVNRFNVAITRAKIGILCIMSDRDLYD"
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SARS coronavirus TW-GD3 isolate TW-GD3_SC18 replicase 1B gene,
partial cds.
       VRL 28-FEB-2004
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Viruses; SRNA positive-strand viruses, no DNA stage; Nidovirales; Coronavirus TW-GD3
Viruses; SRNA positive-strand viruses, no DNA stage; Nidovirales; Coronavirus L Coronavirus.

1 (bases 1 to 626)

Lan,Y.-C., Chen,Y.-J., Lee,C.-M., Liu,T.-T., Lu,J.-J., Chan,Y.-J., Yang,J.-Y., Chen,H.-Y. and Chen,Y.-M.Arthur.

Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS
Unpublished
2 (bases I to 626)
Lan,Y.-C., Chen,Y.-J., Lee,C.-M., Liu,T.-T., Lu,J.-J., Chan,Y.-J., Yang,J.-Y., Chen,H.-Y. and Chen,Y.-M.Arthur.
                                                                                                                                                                                                                                                       Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.

1 (bases 1 to 626)
Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J., Yang, J.-Y., and Chen, Y.-Marthur.

Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 626)
any:'.c.' Chen,Y:-J', Lee,C.-M', Liu,T.-T', Lu,J.-J', Chan,Y.-J.,
Yang,J.-Y., Chen,H.-Y. and Chen,Y.-M.Arthur.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (28-OCT-2003) National Yang-Ming University, AIDS Prevention and Research Center, 155, Li-Nong St., Sec.2, Peitou,
AY451936 626 bp RNA linear VRL 28-FEB SARS coronavirus TW-GD2 isolate TW-GD2_SC18 replicase 1B gene,
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SARS coronavirus TW-GD2
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SQGSEYDFVIFTGTTETAHSCNVNRFNVAITRAKIGILCIMSDRDLYD"
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                                                                                                                                                                                                                                                                              RNA linear VRL 28-FEB-2004
TW-GD5_SC18 replicase 1B gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.

1 (bases 1 to 626)
Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J., Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M. Arthur.
Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS
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Direct Submission
Submitted (28-OCT-2003) National Yang-Ming University, AIDS
Prevention and Research Center, 155, Li-Nong St., Sec.2, Peitou, Taipei, Taiwan 112, R.O.C.
Location/Qualifiers
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SARS coronavirus TW-YM1
SARS coronavirus TW-YM1
Viruses; sRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronavirade; Coronavirus.
1 (bases 1 to 626)
Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J.,
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100.0%; Pred. No. 0.53;
        Pred. No. 0.53;
                                0; Mismatches
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SARS coronavirus TW-GD5 isolate
partial cds.
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Matches 25; Conservative
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7codon start=1
/codon start=1
/product="replicase 1B"
/protein id="AA644823 1"
/db_xref="G1:42741347"
/db_xref="G1:4274147"
/db_xref="G1:42741347"
/db_xref="G1:42747"
/db_xref="G1:42747"
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GVITHDVSSAINRPQIGVVREFLTRNPAWRKAVFISPYNSQNAVASKILGLPTGTVDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J., Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M.Archur.
Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SARS coronavirus TW-GD4
SARS coronavirus TW-GD4
SARS coronavirus TW-GD9
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
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Lan,Y.-C., Chen,Y.-J., Lee,C.-M., Liu,T.-T., Lu,J.-J., Chan,Y.-J.,
Yang,J.-Y., Chen,H.-Y. and Chen,Y.-M.Arthur.
Direct Submission
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                                Yang-Ming University, AIDS
155, Li-Nong St., Sec.2, Peitou,
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/organism="SARS coronavirus TW-GD3"
/wol type="genomic RNA"
/isolate="TW-GD3 SC18"
/db_xref="taxon:264380"
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Direct Submission
Submitted (28-OCT-2003) National Yang
Prevention and Research Center, 155,
Taipei, Taiwan 112, R.O.C.
Location/Qualifiers
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/isolate="TW-GD4_SC18"
/db_xref="taxon:264381"
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EYTNGVCKLMKTIGPDMFLGTCRRCPAEIVDTWSALVYDNKLKAHKDKSGAQCFKMFYK
GVITHDWSSAINRPOIGWYREFLTRPAMRKAVFISFYNSQNAVASKILGLFTQTVDS
SQGSEYDYVIFTQFTFTAHSCNWNRFWAITRAKIGILCIMSDRDLYD"
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1 (bases 1 to 626)

2 (bases 1
Yang,J.-Y., Chen,H.-Y. and Chen,Y.-M.Arthur.
Molecular Epidemiology of SARS in Taiwan - Development of a Simple
Method for Tracing the Origin and Dissemination of SARS
Uppublished
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(Dases 1 to 626)

Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J., Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M.Arthur.

Direct Submission

Submitted (18-007-2003) National Yang-Ming University, AIDS

Prevention and Research Center, 155, Li-Nong St., Sec.2, Peitou, Taipei, Taiwan 112, R.O.C.
                                                                                                                                                                          Lu, J. -J., Chan, Y. -J.,
                                                                                                                                     Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J. Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M. Arthur.

Direct Submission
Submitted (28-OCT-2003) National Yang-Ming University, AIDS
Prevention and Research Center, 155, Li-Nong St., Sec.2, Peitou, Taipel, Taiman 112.
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partial cds.
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/organism="SARS coronavirus TW-YM1"
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100.0%; Pred. No. v...
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/product="replicase 1B"
/protein_id="AAS44826.1"
/db_xref="GI:42741353"
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/protein_id="AAS44827.1"
/db_xref="GI:42741355"
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/isolate="TW-YM2_SC18"
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SARS coronavirus TW-YM3

SARS coronavirus TW-YM3

Viruses, sRNM positive-strand viruses, no DNA stage; Nidovirales;
Viruses, sRNM positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.

1 (bases 1 to 626)

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GVITHDVSSAINRFOIGVVREFLTRNPAMRKAVFISPYNSQNAVASKILGLPTQTVDS
SQGSBYDYVIFTQTTETAHSCNVNRFNVAITRAKIGILCIMSDRDLYD"
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/isolate="TW-YM3_SC18"
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Aas53300 Haemophil Aca34137 Prokaryot Adt 05583 Haemophil Abr11987 E coli ex Aab77024 Human hel Adj39475 Plant cDN Aaf32744 Human sec Aas02416 Human sec Ab190683 Human sec Ab273672 Secreted

Abz 626 Human sec Aby 78121 Human seb Abx 78121 Human eph Abx 25697 Human eph Aby 191662 Human eph Adt 05409 Haemophil Aas 2594 Human cDN Abx 73335 Human con Abx 7335 Human con Abx 7335 Human con Abx 7335 Human con Abx 6359 Human pol Aai 60359 Human pol Aai 60359 Human pol Aai 60360 Human pol

Adm86923 Human pro

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small interfering RNA; siRNA; modified ribonucleotide; viral replication inhibition; hepatitis C virus; HCV; hepatitis C; antiinflammatory; hepatotropic; virucide; hepatitis A virus; hepatitis D virus; hepatitis E virus; Ebola virus; influenza virus; roctavirus; recvirus; poliovirus; human papilloma virus; metapneumoniavirus; coronavirus; viral infection; gene; ds.
                                                                                                                                                                                                        ALIGNMENTS
                                                                                ABZ67269
ABV78121
ABZ35697
                      ABT11987
AAH77024
ABA95848
                                                                                                                      ADT05409
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AAI60359
AAI60358
AAI60360
               ADT05583
                                                                 ABL90683
ABZ73672
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ABL91662
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ABZ34853
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SARS coronavirus
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Aa137976 Probe #66
Aak32125 Human bon
Aak06447 Human bra
Abs31821 Human liv
Abs06892 Human gen
Adr26577 Breast ca
Aca20744 Prokaryot
Ada32694 DNA encod
Acn45080 Mouse gen
Abr12027 E coli ex
Ach26262 Human adu
Ach27372 Human adu
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ba58348 Human foe
ai37976 Probe #66
                                                % Search time 320.703 Seconds
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461.466 Million cell updates/sec
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      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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New RNase resistant small interfering RNA, useful for treating viral infections, e.g., hepatitis C, influenza virus or coronavirus infection.

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Houghton

Seo MY,

Han J,

WPI; 2004-143862/14.

ACA20744 ADA32694 ACN45080

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Example 10; Fig 3; 74pp; English.

Acn50445 Cotton ma Adt05557 Haemophil Abn64132 Human can

ACN50445 ADT05557 ABN64132 AD142255 AD002732 AD062314

Adi42255 Plant tra Ado02732 Rice orth Ado62314 Transcrip

The present invention describes a small interfering RNA (siRNA) which comprises a modified ribonucleotide, where the siRNA is resistant to RNAse and retains the ability to inhibit viral replication. Also described: (1) inactivating a virus in a patient; (2) making a modified siRNA that targets a nucleic acid sequence in a virus; (3) a double-

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begatitis C virus (HCV); (4) inducing targeted RNA interference toward HCV in hepatic cells; (5) inhibiting replication of HCV; (6) a vector comprising a DNA segment encoding the RNA molecule; (7) a host cell comprising the vector of (6); (8) inhibiting replication of HCV in cells carrying HCV; (9) treating hepatitis C in a subject; (10) a modified siRNA molecule comprising a double-stranded RNA molecule of 10-30 uncleotides in length, which mediates RNA interference toward a target agent or virus and is linked to at least one receptor-binding ligand; and (11) inducing targeted RNA interference in a patient. The modified siRNA molecules have antiinflammatorry, hepatorropic and virucide activities.

The modified RNA molecules are useful for inactivating virus in mammalian cells. The siRNAs are useful for treating hepatitis C virus, hepatitis D virus, hepatitis E virus, Ebola virus, inammalian virus, rotavirus, recovirus, poliovirus, human papilloma virus, metapneumoniavirus or coronavirus infections. The methods of the anormalities involved in conferring susceptibility to viral infections in patients. The present sequence represents the SARS coronavirus mucleotide sequence,
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stranded RNA molecule of 10-30 nucleotides that inhibits replication of
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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Pred. No. 0.19;
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2000US-0234687P.
2000US-0236359P.
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100.0%;
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Best Local Similarity 100.
Matches 25; Conservative
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30-JUN-2000;
03-AUG-2000;
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27-SEP-2000;
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human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                                                      Sequence 493 BP; 182 A; 71 C; 70 G; 170 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                    Score 18.6; DB 4;
Pred. No. 1.1e+02;
0; Mismatches 4;
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Pred. No. 1.1e+02;
0; Mismatches 4;
                                                                                                                                                             at ftp.wipo.int/pub/published_pct_sequences
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; 2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
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84.0%;
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ilarity 84.0%;
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Best Local Similarity 84.0'
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tes 21; Conserv
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04-OCT-2000;
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21-SEP-2000;
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The invention relates to a single exon nucleic acid probe for measuring

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Query Match
Best Local Similarity
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                                             Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
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                                                                                                                                                                                                                            Human bone marrow expressed single exon probe SEQ ID NO: 6682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 493 BP; 182 A; 71 C; 70 G; 170 T; 0 U; 0 Other;
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CAGAACACAGTATCTTCCAAAATCT 174
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00532466.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
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nes 21; Conservative
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                                                                                                                                                                                                                                                                   bone marrow
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Single exon nucleic acid probes for analyzing gene expression in human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 4; SEQ ID NO 6438; 650pp + Sequence Listing; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 493 BP; 182 A; 71 C; 70 G; 170 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 18.6; DB 4;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human liver single exon probe, SEQ ID No 6811.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAGAACACAGTATCTTCCAAAATCT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAGAACGCTGTAGCTTCAAAATCT 25
                                                                                                                                                                                                                                                                                                                                                                        Rank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                           (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                        Chen W,
                                                                                                                   30-JUN-2000; 2000US-00608408.

03-AUG-2000; 2000US-005336.

21-SEP-2000; 2000US-0234687P.

27-SEP-2000; 2000US-0236359P.
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26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
                                                                                                                                                                                                                                              04-OCT-2000; 2000GB-00024263.
30-JAN-2001; 2001WO-US000667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 74.4%;
l Similarity 84.0%;
21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001WO-US000664
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABS31821 standard; DNA; 493
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                                                                                                                                                                                                                                                                                                                                                                        Penn SG, Hanzel DK,
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21-OCT-2004 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                             Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
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à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                              The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABS25011-ABS51005 represent human liver single exon nucleic acid probes of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                         Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; ds; single exon probe; asthma; lung cancer; COPD; ILD; chronic obstructive pulmonary disease; interestitial lung disease; familial idiopathic pulmonary fibrosis; neurofibromatosis; tuberous sclerosis; gaucher's disease; Niemann-Pick disease; Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosidarosis; pulmonary historycosis; lymphangloleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dyskinesis; pulmonary hypertension;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human genome-derived single exon probe from lung SEQ ID No 6883.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.4%; Score 18.6; DB 4; Length 493; 84.0%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 493 BP; 182 A; 71 C; 70 G; 170 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 6811; 658pp; English
                                                                                                                                 Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25
                                                                                                                                                                                                                             gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 CAGAACGCTGTAGCTTCAAAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP
                                                                                              (MOLE-) MOLECULAR DYNAMICS INC
                 21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2001; 2001WO-US000665.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000; 2000US-0180312P.
26-MAY-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
   03-AUG-2000; 2000US-00632366.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 84.01
Local 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           primary ciliary dyskines
hyaline membrane disease
                                                                                                                                 Hanzel DK,
                                                                                                                                                                      WPI; 2001-488898/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200186003-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19-AUG-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABS06892;
                                                                                                                                 Penn SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 7
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The invertion relates to a spatially accression in a sample extruction uncleic acid probes for measuring gene expression in a sample derived from human lung comprising single exon nucleic acid probes having one of from human lung comprising single exon nucleic acid probes having one of 126f4 unucleic acid sequences mentioned in the specification, or their complements or the 12387 open reading frames derived from the 126f4 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic acid expressed in the human lung, measuring gene expression in a sample derived from human lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably content and a enkaryote; and the paper and the detectably belief or a single exon probe, comprising (a) identifying exons in a evant from genomic sequence by the method above mentioned microarray; assigning exons to a single exon probe, comprising (a) identifying exons from genomic sequence by the method above and (b) measuring the expression of each of the exons in the tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the tissues and/or cell types indicates that the exons should be assigned to a single gene; a peptide comprising one of 12011 sequences, mentioned in the specification, or encoded by the probes/open reading frames (ORP). The probes such as asterma, lung expression of deterived munk and for the study of lung diseases such as asterma, lung disease (TLD), familial idiopathic pulmonary fibrosis, encodible releases or lung derived munk and for the sequence bulmonary fibrosis, encodible and expression of the expression of the expression of the express
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spatially-addressable set of single exon nucleic acid probes, used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 493 BP; 182 A; 71 C; 70 G; 170 T; 0 U; 0 Other;
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Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      measure gene expression in human lung samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 6883; 634pp; English.
                                                                                                                                                                                                                                                                                                       Chen W, Rank DR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 CAGAACACAGTATCTTCCAAAATCT 174
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                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0236359P.
04-OCT-2000; 2000GB-00024263.
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84.0%;
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                                                                                                                                                                                                                                                                                                       Hanzel DK,
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screening

Zyskind JW; Xu HH;

Homo sapiens

05-AUG-2004.

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The invention relates to an isolated nucleic acid comprising any one of the foll antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a proincter operably linked to the nucleic acid models acid; (2) a host cell containing the vector; (3) an isolated polypeptide acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide or its fragment whose expression is inhibited by the compound that influences the activity of gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, or that inhibits proliferation or the biological pathway required for proliferation-required gene or its gene product lies to a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound,'s activity; (11) a culture comprising strains in which the gene or proliferation of the strains is present in a culture or collection of the strains; or (13) identifying the target of a compound that inhibits the strains; or (13) identifying the target of a compound that inhibits the contains or collection of an organism. The antisense nucleic acids are useful for interior in antificial acids are useful for interior in antification or the useful for interior and in a culture or collection of an organism. The antisense nucleic acids are useful for interior in an expension or the useful for interior in the expension or the useful for interior in a collection or inter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ds; gene; Acinetobacter baumannii; bacterial disease; antibacterial;
                                                                                                                                                                                                                                                                                                                                                                    for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1524;
                                                                                                                                                                                                                                                                                                                                          proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 17.8; DB 8; Length 1: Pred. No. 3.1e+02;
                                                                                                                                                                     Ohlsen KL,
Forsyth RA,
                                                                                                                                                                                                                                                                                                                                    New antisense nucleic acids, useful for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA encoding Acinetobacter baumannii protein #3981
                                                                                                                                                                     Haselbeck R,
Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 14; SEQ ID NO 8614; 1766pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                     Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADA32694 standard; DNA; 1569 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 ACCCTGTAGCTTCAAAAATCT
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.2%;
90.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                (ELIT-) ELITRA PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19; Conservative
                                                                                                                                                                     Zamudio C,
Trawick JD,
                                                                                                                                                                                                                                                    WPI; 2003-029926/02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
                                                                                                                                                                                                                                                                                     P-PSDB; ABU16874.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                     Wang L,
Wall D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a method of classifying a breast cancer patient according to prognosis by determining the similarity between the level of expression of each of five genes for which markers are listed in the specification, in a cell sample taken from the breast cancer patient, to control levels of expression for each respective five genes to obtain a patient similarity value. The methods are useful for classifying a breast cancer patient according to prognosis. Kits and computer program products are useful for data analysis using the diagnostic, prognostic and statistical methods of the invention. This sequence corresponds to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Classifying a breast cancer patient according to prognosis comprises determining the similarity between the level of expression of each of five genes in a cell sample taken from patient, to control levels.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72.8%; Score 18.2; DB 13; Length 1056; 87.0%; Pred. No. 1.9e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antisense; ds; prokaryotic essential gene; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1056 BP; 389 A; 168 C; 167 G; 332 T; 0 U; 0 Other;
                                                                                  ds; breast cancer; prognosis; gene expression; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 2438; 226pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         marker used in the method of the invention.
                             cancer prognosis marker #2438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAACGCTGTACCTTTAAAAATTT 967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 GAACGCTGTAGCTTCAAAATCT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prokaryotic essential gene #2401.
                                                                                                                                                                                                                                                                                                                                                                                                                       (ROSE-) ROSETTA INPHARMATICS LLC (NECA-) NETHERLANDS CANCER INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВР
                                                                                                                                                                                                                                                                                                                                                                  15-JAN-2003; 2003US-00342887.
                                                                                                                                                                                                                                                                                                         15-JAN-2004; 2004WO-US001100
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06-SEP-2001; 2001US-00948993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      19-JUN-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Van't Veer LJ, He Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2004-593473/57.
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Gaps

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WO200277183-A2

ACA20744;

RESULT

Query Match Matches

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03-OCT-2002

04-JUN-1999;

09-JUN-1998;

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Breton

plants.

US6562958-B1

13-MAY-2003

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The invention relates to a method for preparing a gene that lacks CpG but is still expressible in Escherichia coli by synthesis of a polynucleotide sequence, encoding a protein expressible in E. coli but lacking the codons NCG, CGN or NTA (N = any of A, C, G or T) or any codons that end in C when the following codon starts with G. The CpG lacking genes are especially useful as selection (antibiotic resistance) or marker (lacZ) genes, but they (also CpG-free promoters, transcription units, origins of replication, plasmids and cells for replication of the plasmids) can be used for transformation, for biotechnological or medical purposes, e.g.
                                                                                                                                                           are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vii) for inhibiting the activity of CAP; (vii) for treating carcinoma; (vii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent
                   Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Preparing gene with no cytosine methylation, useful e.g. for expressing proteins in Escherichia coli, by selecting codons to avoid presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 83836 BP; 23536 A; 15199 C; 15996 G; 26941 T; 0 U; 2164 Other;
                                                                                                                                    present invention relates to novel DNA and protein sequences which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CpG; Escherichia coli; expression; DNA vaccine; gene therapy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17.8; DB 11; Length 83836;
Pred. No. 5.2e+02;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E coli expressible CpG deprived gene related oligo SEQ ID No
                                                                                           Claim 1; SEQ ID NO 1849; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16018 AGAACCCTGTAGCTTTAAAAA 15998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AGAACGCTGTAGCTTCAAAA 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure, Fig 4; 152pp; French.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 71.2%;
1 Similarity 90.5%;
19; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
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CpG dinucleotides.
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ABT12027/c
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                                                                                                                                                                                                                                                                                                                                                                                                                        New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to isolated Acinetobacter baumannii nucleic acids. The A. baumannii nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for plants. The present sequence represents DNA encoding an A. baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1569 BP; 461 A; 331 C; 352 G; 425 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatic; carcinoma; lymphoma; cancer; murine; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; SEQ ID NO 3981; 328pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1499 ACGCAGTAGCTCCAAAAATCT 1519
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                                                                                                                                                                                                                                                             (GENO-) GENOME THERAPEUTICS CORP.
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                                                                                                                                                               99US-00328352
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                                                                                                                                                                                                              98US-0088701P
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90.5%;
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Best Local Similarity 90.5.
Best Local Similarity 90.5.
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                      Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                     2003-576092/54.
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                                                                                                                                                                                                                                                                                                            Bush D;
                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-576092/
P-PSDB; ADA36820.
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protein.

Mus musculus.

12-SEP-2003

Morris DW;

18-NOV-2004

ACN45080;

ACN45080/c RESULT 11

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Gaps

segdata.uspto.gov/sequence.html?DocID=20030073623

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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the technique of SBH (sequencing by Pybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences cuestil in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probbes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisenses DNA or RNA. The purified polypeptide is useful for generating antisease process. Sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA libraries, useful
chromosome and gene
or in generating
they are particularly well suited for preparation of DNA vaccines for un humans or animals. The polymucleotides of the invention can be used for treating disorders by gene therapy. This polymucleotide sequence represents an oligonucleotide relating to the Escherichia coli expressible CpG gene of the invention
                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jones LW;
                                                                                                                                              Score 17.6; DB 6; Length 60; Pred. No. 2.5e+02;
                                                                                                                                                                                   4; Indels
                                                                                                             Sequence 60 BP; 19 A; 13 C; 14 G; 14 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dickson MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polynucleotide sequences obtained from various as hybridization probes, as oligomers for PCR, for mapping, in the recombinant production of protein,
                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 13474; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stache-Crain B,
                                                                                                                                                                                                                      1 CAGAACGCTGTAGCTTCAAAATC 24
                                                                                                                                                                                                                                                  24
                                                                                                                                                                                                                                          47 CAGAACATTGTTGCTTCCAAAATC
                                                                                                                                                                                                                                                                                                                                                   ACH26262 standard; cDNA; 487 BP.
                                                                                                                                               70.4%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human adult ovary cDNA #4642.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUL-2001; 2001US-00918995.
                                                                                                                                                                                                                                                                                                                                                                                                                           13-OCT-2003 (first entry)
                                                                                                                                                                 Local Similarity 83.3
ses 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LABAT I.
STACHE-CRAIN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drmanac RT, Labat I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antisense DNA or RNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DRMANAC R T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (LABA/)
(STAC/)
(DICK/)
(JONE/)
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                                                                                                                                                                                                                                                                                                           RESULT 13
                                                                                                                                                                                                                                                                                                                                ACH26262
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The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was determined by the tecchnique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, or chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense by a crown or the sequence is useful for generating antisense by sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                   Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating
                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jones LW;
                                                                       Length 487;
                                 Sequence 487 BP; 123 A; 107 C; 139 G; 114 T; 0 U; 4 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 487 BP; 122 A; 105 C; 139 G; 117 T; 0 U; 4 Other;
                                                                                                       4; Indels
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                                                                   Score 17.6; DB 9;
Pred. No. 3.38+02;
0; Mismatches 4;
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                                                                                                                                                                             281 CAGCAGGCTGTAGCTCCAAAATTC 304
                                                                                                                                           24
                                                                                                                                           1 CAGAACGCTGTAGCTTCAAAATC
                                                                                                                                                                                                                                                                      ACH27372 standard; cDNA; 487 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUL-2001; 2001US-00918995.
                                                                                                                                                                                                                                                                                                                                                                                 Human adult ovary cDNA #5752.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-JUL-2001; 2001US-00918995
                                                                   Query Match
Best Local Similarity 83.3%;
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DRMANAC R T.
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                                                                                                                                                                                                                                                                                                                                              13-OCT-2003
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                                                                                                                                                                                                                                                                                                          ACH27372;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (JONE/)
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Query Match 70.4%; Score 17.6; DB 9; Length 487; Best Local Similarity 83.3%; Pred. No. 3.38+02; Matches 20; Conservative 0; Mismatches 4; Indels (
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1 CAGAACGCTGTAGCTTCAAAATC 24

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280 CAGCAGCTGTAGCTCCAAAATTC 303

ACN50445/c ID ACN50445 standard; cDNA; 562 BP.

ACN50445;

(first entry) 02-DEC-2004

Cotton mature seed EST Clone ID: LIB3827-001-Q1-K6-G12, SEQ:5226.

Cotton; plant; EST; expressed sequence tag; transgenic plant; seed; variety Coker 312 Boswell 96 Field; library Libs27; molecular tag; molecular marker; genetic mapping; molecular mapping; seed germination; plant growth; plant quality; plant yield; plant breeding; tissue printing; ss

Gossypium hirsutum

US2004123340-A1.

24-JUN-2004.

12-DEC-2001; 2001US-00021323.

14-DEC-2000; 2000US-0255619P

(DEIK/) DEIKMAN J. (FENG/) FENG P C C. (FINC/) FINCHER K L. (ZIEG/) ZIEGLER T E.

Deikman J, Feng PCC,

Ziegler TE;

Fincher KL,

WPI; 2004-479808/45.

New isolated nucleic acid molecule that encodes a plant protein or its fragment, useful for isolating a variety of agronomically significant genes associated with plant growth, quality or yield, and as molecular tags to map genes.

Claim 1; SEQ ID NO 5226; 34pp; English.

The invention relates to 17880 cotton expressed sequence tags (BSTs;

ACNA5220-ACN63099). The ESTs were isolated from cDNA libraries generated

CC ACNA5220-ACN63099). The ESTs were isolated from cDNA libraries generated

CC ACNA5220-ACN63099). The ESTs were isolated from cDNA libraries generated

CC ACNA5220-ACN63099). The ESTs were isolated from variety developing fibres, carpel walls and septa from variety

Nucotton33B. The invention also relates to substantially purified

CC Nucotton33B. The invention also relates to substantially purified

CC Invention, and to transformed plants having a nucleic acid molecules of the

CC Invention, and to transformed plants having a nucleic acid construct

CC COMPACIANT tags to isolate genetic regions, to isolate genes, to map

CC Genes, to determine gene function and to determining whether genes are

CC CC Members of a particular gene family. The nucleic acid molecules may be

CC Used for isolated with plant growth, quality, yield, and could also serve as

CC links in metabolic and catabolic pathways. The nucleic acid molecules are

CC also useful for identifying genes important in initiating and maintaining

CC also actual for identifying genes important in initiating and maintaining

CC also actual for identifying genes important in initiating and acid-regulatory elements which will be useful to express

CC during seed germination. The ESTs additionally enable the acquisition of promoters and cis-regulatory elements which will be useful in breeding

CC addition genetic and molecular markers useful in breeding

CC ACHOMIST SCHORES ACHOMIST ACHOMIST

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0
significant genes. The nucleic acid molecules are further useful for detecting the expression level or pattern of a protein or mRNA and for detecting the presence or quantity of a protein by tissue printing. The present sequence represents a specifically claimed EST isolated from a cotton variety Coker 312 Boswell 96 Field mature seed cDNA library [LIB3827]. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                         ;
0
                                                                                                                                                                                                                                                             Length 562;
                                                                                                                                                                                                                     Sequence 562 BP; 170 A; 114 C; 139 G; 138 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                         seqdata.uspto.gov/sequence.html?DocID=US20040123340
                                                                                                                                                                                                                                                             DB 13;
                                                                                                                                                                                                                                                             Score 17.6; DB 13
Pred. No. 3.3e+02;
0; Mismatches 4.
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Search completed: May 16, 2005, 01:09:16 Job time : 325.703 secs

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Sequence 3981, Ap Sequence 610, App Sequence 610, App Sequence 16, Appl Sequence 16, Appl Sequence 459, App Sequence 461, Appl Sequence 33, Appl Sequence 1, Appl Sequence 1, Appli Sequence 1, Appli
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Sequence 24852, A
Sequence 12660, A
Sequence 13131, A
Sequence 16108, A
Sequence 1, Appli
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Sequence 22401, A
Sequence 26775, A
Sequence 26776, A
                                                                              May 16, 2005, 00:11:05; Search time 93.5547 Seconds (without alignments) 437.251 Million cell updates/sec
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*
(cgn2_6/ptodata/1/ina/5B_COMB.seq:*
(cgn2_6/ptodata/1/ina/6A_COMB.seq:*
(cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
5.1.6
Compugen Ltd.
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US-09-328-352-3981
US-09-949-016-630
US-08-49-645A-16
US-08-702-367A-16
PCT-US95-04681-16
US-09-620-312D-459
US-09-620-312D-461
US-09-620-312D-461
US-09-620-312D-461
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US-09-438-185A-1

US-09-270-767-9570

US-09-949-016-12660

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US-09-949-016-10108

US-09-948-016-10108
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US-09-643-990A-1
US-09-949-016-13904
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US-09-949-016-26775
US-09-949-016-26776
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                                                                                                                                                                                                                                                  1202784 seqs, 818138359 residues
                                                                                                                                                                          1 cagaacgctgtagcttcaaaaatct 25
GenCore version
Copyright (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
                                                       - nucleic search, using sw model
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25
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Match Length DB
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Sequence 17375, Application US/09949016

Fatent No. 6812339

GENERAL INPORMATION:
THE SET OF LINEANTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
FRIOR PELLING DATE: 2000-04-14
FRIOR PELLING DATE: 2000-10-20
FRIOR PELLING DATE: 2000-10-20
FRIOR PELLING DATE: 2000-10-3
FRIOR PELLING DATE: 2000-10-3
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 17375
LENGTH: 84296
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
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                             Sequence 26778, p. Sequence 31117, Sequence 31117, Sequence 34598, Sequence 54630, Sequence 61461, Sequence 119063, Sequence 119063, Sequence 119063, Sequence 119155, Sequence 
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142039,
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                    US-09-949-016-26778

US-09-949-016-31117

US-09-949-016-31117

US-09-949-016-54598

US-09-949-016-54630

US-09-949-016-54661

US-09-949-016-119027

US-09-949-016-119099

US-09-949-016-119099

US-09-949-016-119135

US-09-949-016-119135

US-09-949-016-119207

US-09-949-016-119207

US-09-949-016-119207

US-09-949-016-119207

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Pred. No. 83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1) ... (84296)
; OTHER INFORMATION: n = A, T, C or G
US-09-949-016-17375
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87.0%;
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Best Local Similarity 87.0'
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; Sequence 630, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: 2000-40-14
; PRIOR APPLICATION NUMBER: 60/231, 768
; PRIOR PILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-10-03
; PRIOR PLING DATE: 2000-09-08
; NUMBER OF SECIENCE PRIOR WINDER: 60/231, 498
; NUMBER OF SECIENCE PRIOR WINDER: 2007012
; SEQIENCE PRIOR PRIOR
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Sequence 4030, Application US/09949016

Sequence 4030, Application US/09949016

Sequence 4030, Application US/09949016

Sequence 4030, Application US/09949016

SEQUENCE TO THE NORMATION:

TITLE OF INVENTION: POLIYORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 50/241,755

PRIOR PLILING DATE: 2000-10-20

PRIOR PLILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PLILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-10-03

PRIOR PLILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRASEQ for Windows Version 4.0
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Best Local Similarity 90.5%; Pred. No. 56;
Matches 19; Conservative 0; Mismatches 2;
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Best Local Similarity 83.3%; Pred. No. 88;
Matches 20; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                 5 ACGCTGTAGCTTCAAAAATCT 25
                                  ; LENGTH: 1569
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-3352-3981
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; ORGANISM: Human
US-09-949-016-630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-949-016-4030
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LENGTH: 4522
SEQ ID NO 3981
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4; Length 4523;
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Patent No. 5981246
GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMGEN Patent Operations/RBW
STREET: 1840 Dehavilland Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                             ### Sequence 16, Application US/08449645A

| Sequence 16, Application US/08449645A
| Patent No. 5981245
| GENERAL INFORMATION:
| APPLICANT: Fox, Gary M. APPLICANT: Fox Gary M. TITLE OF INVENTION: EMP-Like Receptor Protein Tyrosine; TITLE OF INVENTION: Kinases
| NUMBER OF SEQUENCES: 43
| CORRESPONDENCE ADDRESS: | CORRESPONDENCE A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/449,645A
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         DB
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Pred. No. 88;
0; Mismatches
    Query Match 70.4%; Score 17.6; D
Best Local Similarity 83.3%; Pred. No. 88;
Matches 20; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Amgen Patent Operations/RBW
STREET: 1840 Dehavilland Drive
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/ DOCKET NUMBER: A-2
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 4529 base pairs
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70.4%;
Best Local Similarity 83.3%;
Matches 20; Conservative (
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STATE: California
COUNTRY: USA
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US-08-449-645A-16
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                      Length 4529;
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                      DB 5;
                    Score 17.6; D
Pred. No. 88;
0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR APPLICATION NUMBER: 09/488,725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17.6;
Pred. No. 94
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Sequence 459, Application US/09620312D
Patent No. 6569662
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Patent No. 6569662
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NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pt FL_genes Version 1.0
                    70.4%;
ilarity 83.3%;
Conservative
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Best Local Similarity 83.3%;
Matches 20; Conservative
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Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
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Zhou, Ping
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Wehrman, Tom
Xue, Aidong J
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Liu, Chenghua
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Ma, Yunqing
     Query Match
Best Local Similarity
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Zhang, Jie
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US-09-620-312D-459
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NAME/KEY: CDS
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GENERAL INFORMATION:
APPLICANT: Fox, Gary M.
TITLE OF INVENTION: EPH-Like Receptor Protein Tyrosine
TITLE OF INVENTION: Kinases
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Patent Operations/RBW
           ZIP: 91320
ZIP: 91320
MEDIUM TYPER READABLE FORM:
MEDIUM TYPER PROPERTION GISK
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,367A
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CURRENT APPLICATION DATA:
PLILCATION NUMBER: PCT/US95/04681
FILING DATE:
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70.4%; Score 17.6;
Best Local Similarity 83.3%; Pred. No. 86
Matches 20; Conservative 0; Mismatche
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                              NAME: Winter, Robert B.
RREREBNEA/DOCKET NUMBER: A-:
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 4529 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 16
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320
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EDNESS: single
                                                                                                                                                         FILING DATE:
CLASSIFICATION: 435
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; LOCATION: 186
US-08-702-367A-16
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LOCATION: 186

PCT-US95-04681-16
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COUNTRY:
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: 13206 base pairs
nucleic acid
EDNESS: double
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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                                                                                                                                                      Best Local Similarity 83.3
Matches 20; Conservative
                                ORGANISM: Homo sapiens
                                                                  ; NAME/KEY: CDS
; LOCATION: (59)..(4291)
US-09-620-312D-460
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Best Local Similarity
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STATE: Maryland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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US-08-961-527-33/c
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LENGTH: 6382
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                                                                                                                                        Query Match
                 TYPE: DNA
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CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR FILING DATE: 2000-04-25
NUMBER: OF SEQ ID NOS: 1105
SOFTWARE: Pt-Lgenes Version 1.0
SEQ ID NO 460
                                                                                                                                               APPLICANT: Commanacy, Radoje T.
TITLE OF INVENTION: No. 656962el Nucleic Acids and
TITLE OF INVENTION: No. 656962el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
TITLE OF INVENTION: Polypeptides
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR PELICATION NUMBER: 09/552,317
PRIOR PELICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: PL_genes Version 1.0
SEQ ID NO 461
LENGTH: 6304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drmanac, Radoje T.
                                                                                                      Wang, Dunrui
Wang, Zhiwei
John Tillinghast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang, Zhiwei
John Tillinghast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Asundi, Vinod
Zhang, Jie
Ren, Feiyan
Chen, Rui-hong
Zhao, Qing A.
Wehrman, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 83.3
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Yang, Yonghong
Wang, Jian-Rui
Zhou, Ping
Ma, Yunging
                                   Yang, Yonghong
Wang, Jian-Rui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
                   Kue, Aidong J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kue, Aidong J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wang, Dunrui
                                                                                    Ma, Yunqing
                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .. (4213)
                                                                       Ping
                                                                       Zhou'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-620-312D-460
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; NAME/KEY: CDS
; LOCATION: (59)
US-09-620-312D-461
                                                                                                                                      APPLICANT:
APPLICANT:
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APPLICANT:
                                                                                    APPLICANT:
APPLICANT:
APPLICANT:
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Sequence 33, Application US/08961527
Patent No. 6420135
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
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0
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  DB 4; Length 6382;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 70.4%; Score 17.6; DB 3;
83.3%; Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                            0; Mismatches
70.4%; Score 17.6;
83.3%; Pred. No. 95;
                      Pred. No.
                                                                                                                             3819 cagcagcrcradecrccadarrc 3842
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                                                                                       1 CAGAACGCTGTAGCTTCAAAAATC 24
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US-09-557-884-1/c
; Sequence 1, Application US/09557884
; Patent No. 6506581
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNATY AGENT INFORMATION:
NAME: BYCOKES, A. Anders
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB34
TELEPHONE: (301) 309-8504
TELEPHONE: (301) 309-8512
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISIES:
LENGTH: 13206 base pairs
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/643,990A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     519422 AGAACGCTGTTCAATCAAAATCT 519399
                                                                                            FILING DATE: 23-Aug-2000
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
         OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30403 AGAAAGCTGTAGCCTGAAAAT 30424
                                                                                                                                                                                                                                                                             NAME: Kenley K. Hoover
REGISTRATION NUMBER: 40,310
REFERENCE/DOCKET NUMBER: PB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1830121 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Sequence 1, Application US/09198452A
                                                                                                                                                                                                                                FILING DATE: 1995-04-21 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 301-610-5790
                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 310-309-8439 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 68.8%;
Best Local Similarity 86.4%;
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 83.3
Matches 20; Conservative
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US-09-198-452A-1
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APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hamilton O. Smith
J. Craig Venter
TITLE OF INVENTION: The Nucleotide sequence of the Hamophilus influenzae Rd Genome, Fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.4%; Score 17.6; DB 4; Length 1830121; 83.3%; Pred. No. 2.6e+02; Live 0; Mismatches 4; Indels 0; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thereof, and Uses Thereof
                                                                                        NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Human Genome Sciences, Inc
                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/557, 884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB186P3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: 3 1/2 inch diskette COMPUTER: Dell Pentium
                                                                                                                                                                                                                                                                                                MEDIUM TYPE: 3 1/2 inch diskette COMPUTER: Dell Pentium OPERATING SYSTEM: MS DOS v6.22 SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     519422 AGAACGCTGTTCAATCAAAATCT 519399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:

APPLICATION UNDBER: 08/476,102
FILING DATE: JUN-5-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 9410 Key West Avenue
CITY: Rockville,
STATE: MD
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Robert D. Fleischmann
Mark D. Adams
Owen White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09643990A Patent No. 6528289 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20850
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 83.33
Matches 20; Conservative
                                                                                                                                                                                  CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERIS
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                                                                                                                                                                                                                                  COUNTRY: USA
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Sequence 13904, Application US/09949016

Patent No. 6812394

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CLOOD.307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-02

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFFWARE: PRESC FOR Windows Version 4.0
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                                                      Gaps
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70.4%; Score 17.6; DB 4; Length 1830121; 83.3%; Pred. No. 2.6e+02; ive 0; Mismatches 4; Indels 0;
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Pred. No. 2.2e+02;
0; Mismatches 3;
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NAME/KEY: misc feature
LOCATION: (37501)...(39000)
CTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (37501)...(40500)
CTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (40501)...(42000)
CTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (42001)...(43500)
CTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (43501)...(45000)
CTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (45001)...(46500)
CTHER INPORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (46501)...(46500)
CTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (48001)...(49500)
CTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (480001)...(51000)
CTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (495001)...(51000)
CTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (510001)...(52500)
CTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (525001)...(54000)
CTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (525001)...(54000)
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INFORMATION: n=a or c or g or t
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LOCATION: (540001)..(555000)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc feature
COCATION: (555001)..(570000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (57001)..(585000)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc_feature
LOCATION: (585001)..(600000)
OTHER INFORMATION: n=a or c or g or
                           OTHER INFORMATION: n=a or c or g or NAME/KEY: misc feature (LCCATION: (300001). (315000) OTHER INFORMATION: n=a or c or g or
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LOCATION: (600001)..(615000)
OTHER INFORMATION: n=a or c or g or
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                                                                                                                                  NAME/KEY: misc feature
LOCATION: (315001)..(330000)
OTHER INFORMATION: n=a or c or g
                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (33001)..(345000)
OTHER INFORMATION: n=a or c or g
                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (34501)..(360000)
OTHER INFORMATION: n=a or c or g
                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (360001)..(375000)
OTHER INFORMATION: n=a or c or g
     (285001)..(300000)
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(615001)..(630000)
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LOCATION: (645001)..(660000)
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LOCATION: (630001)..(6
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Patent No. 6559294

GENERAL INFORMATION:
FAULUANT: Griffais, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, preve
TITLE OF INVENTION: and treatment of infection
FILE REFERENCE: 9710-003-999
CURRENT FILINGATE: 1999-11-24
NUMBER OF SEQ ID NOS: 6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (30001)..(45000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (45001)..(60000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (60001)..(75000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (75001)..(90000)
OTHER INFORMATION: n=a or c or g or t
OTHER INFORMATION: n=a or c or g or t
OTHER INFORMATION: 09000)
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LOCATION: (15001)..(16500)
OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc_feature
LOCATION: (16501)..(18000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (270001)..(285000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (120001) .. (135000)
OTHER INFORMATION: n=a or c or g
NAME/KEY: misc feature
LOCATION: (135001) .. (150000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (18000)...(195000)
OTHER INFORMATION: n=a or c or g
NAME/KEY: misc feature
LOCATION: (195001)...(210000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (22501)..(240000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (90001)..(105000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (105001)..(120000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (25501)..(270000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (15001)..(30000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (24001)..(255000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (1)...(15000)
OTHER INFORMATION: n=a or c or
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LOCATION: (210001)..(225000)
OTHER INFORMATION: n=a or c or
                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Chlamydia pneumoniae
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                                                                                                                                                                                                                                                                    SEQ ID NO 1
LENGTH: 1230025
                                                                                                                                                                                                                                                                                                                            TYPE: DNA
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INFORMATION: n=a or c or g or t

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Ouery Match 68.8%; Score 17.2; DB 4; Length 1230025; Best Local Similarity 86.4%; Pred. No. 3.8e+02; Matches 19; Conservative 0; Mismatches 3; Indels 0; C
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LOCATION: (765001)..(780000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (78000)..(795000)
OTHER INFORMATION: n=a or c or g or t
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LOCATION: (870001)..(885000)
OTHER INFORMATION: n=a or c or g or t
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OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc_feature
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LOCATION: (795001)..(810000)
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LOCATION: (840001)..(855000)
OTHER INFORMATION: n=a or c or g or t
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OTHER INFORMATION: n=a or c or g or t
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OTHER INFORMATION: n=a or c or g or t
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OTHER INFORMATION: n=a or c or g or t
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OTHER INFORMATION: n=a or c or g or
NAME/KEY: misc_feature
LOCATION: (750001)..(765000)
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LOCATION: (825001)..(840000)
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                                          NAME/KEY: misc feature
LOCATION: (675001)..(690000)
OTHER INFORMATION: n=a or c or g or
                                                                                                                  NAME/KEY: misc feature
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OTHER INFORMATION: n=a or c or g or
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LOCATION: (720001)..(735000)
OTHER INFORMATION: n=a or c or g or
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LOCATION: (810001)..(825000)
OTHER INFORMATION: n=a or c or g or
ON: (660001)..(675000)
INFORMATION: n=a or c or g or
                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (70501)..(72000)
OTHER INFORMATION: n=a or c or g
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LOCATION: (855001)..(870000)
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Search completed: May 16, 2005, 06:11:23 Job time : 101.555 secs

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GenCore version 5.1.6
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- nucleic search, using sw model OM nucleic

May 16, 2005, 02:00:36 ; Search time 1185.16 Seconds (without alignments) 129.102 Million cell updates/sec Run on:

US-10-808-187A-2471 25 1 cagaacgctgtagcttcaaaaatct 25 Title: Perfect score:

Sequence:

IDENTITY NUC Gapext 1.0 Scoring table:

11324664 Total number of hits satisfying chosen parameters:

5662332 seqs, 3060109652 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

Published_Applications_NA:* Database :

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/cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:* 'pubpna/US10_NEW_PUB.seq Cgm2_6/1

Cgm2_6/1 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Sequence 2471, Ap	11, Appl	, Appli	, Appli	, Appli	, Appli	', Appli	5, Appl	, Appli	Appli	. Appli
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Description	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Segmence
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, B	19	19	19	19	19	19	19	18	18	19	19
% Query Match Length DB ID	25	1213	5262	28920	28920	29291	29430	29727	29727	29727	29727
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
Score	25	25	25	25	25	25	25	25	25	25	25
Result No.	1	7	٣	4	2	9	7	80	6	10	11

	110111	Sequence 67, Appl Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1, Appli Sequence 11173, A Sequence 2438, Ap Sequence 2438, Ap	1849, AE 1849, AE 1849, AE 18474, AE 18474, AE 18474, AE 18476, AE 18476, AE 1845, A
0.839-729-17 0.889-447-9 0.699-936-3 0.839-729-16 0.808-187-15 0.808-187-16	0-808-187-1 0-808-187-1 0-808-187-1 0-808-187-1 0-889-447-1 0-839-729-1	US-10-626-879-67 US-10-889-447-1 US-10-889-447-2 US-10-699-936-2 US-10-808-187-1 US-09-864-761-11173 US-10-172-118-2438 US-10-172-118-2438 US-10-342-887-2438	US-110-087-192-1849 US-10-469-851-48 US-09-783-59-918-988 US-09-918-995-13474 US-10-021-323-526 US-10-021-323-526 US-10-027-632-24526 US-10-027-632-24526 US-10-10-74-788-718 US-10-424-599-81579
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ALIGNMENTS

APPLICANT: NICHOLLS, JOHN
TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
TITLE OF INVENTION: RESPIRATORY SYNDROME (SARS) FILE REFERENCE: V9661.0078 CURRENT APPLICATION NUMBER: US/10/808,187 CURRENT FILING DATE: 2004-03-24 CURRENT FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: 60/457,031
PRIOR APPLICATION NUMBER: 60/457,031
PRIOR APPLICATION NUMBER: 60/457,730
PRIOR PILING DATE: 2003-03-26
PRIOR FILING DATE: 2003-04-02
PRIOR FLING DATE: 2003-04-02
PRIOR PELING DATE: 2003-04-03
PRIOR PELING DATE: 2003-04-03
PRIOR PILING DATE: 2003-04-03
PRIOR PILING DATE: 2003-04-08
PRIOR PILING DATE: 2003-04-09
PRIOR PILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: 60/462,805
PRIOR APPLICATION NUMBER: 60/464,805
PRIOR APPLICATION NUMBER: 60/464,806
PRIOR PILING DATE: 2003-05-05
PRIOR PILING DATE: 2003-04-03
PRIOR PILING DATE: 2003-04-03
PRIOR PILING DATE: 2003-05-05
PRIOR PILING DATE: 2003-04-23
PRIOR PILING DATE: 2003-04-23
PRIOR PILING DATE: 2003-04-23
PRIOR PILING DATE: 2003-04-23 Sequence 2471, Application US/10808187 Publication No. US2005000900941 GENERAL INFORMATION: APPLICANT: PEIRIS, JOSEPH S. APPLICANT: YURB, KWOK YUNG APPLICANT: POON, LIT MAN APPLICANT: GUAN, YI POON, LIT MAN GUAN, YI CHAN, KWOK HUNG APPLICANT: APPLICANT:

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Sequence 9, Application US/10699936; Publication No. US20050095582A1; GENERAL INFORMATION:
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NAME/KEY: misc_feature
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LENGTH: 5262
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APPLICANT: CHAN, TWOK HUNG
APPLICANT: CHAN, KWOK HUNG
APPLICANT: CHAN, KWOK HUNG
APPLICANT: CHAN, KWOK HUNG
APPLICANT: NICHOLLS, OGN
TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
TITLE OF INVENTION: A DIAGNOSTIC ASSAY
FILE REFERENCE: V9661.0078
CURRENT APPLICATION NUMBER: 60/457,031
PRIOR APPLICATION NUMBER: 60/457,031
PRIOR APPLICATION NUMBER: 60/459,931
PRIOR APPLICATION NUMBER: 60/459,931
PRIOR PELLOR DATE: 2003-04-02
PRIOR PILING DATE: 2003-04-03
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; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-808-187-2471
                                                                                                                                                                                                                                                                                                                               100.0%; Score 25; DB 19; Length 25; 100.0%; Pred. No. 0.071; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11, Application US/10808187
Publication No. US20050009009A1
GENERAL INFORMATION:
APPLICANT: PEIRIS, JOSEPH S. M.
APPLICANT: YUEN, KWOK YUNG
APPLICANT: POON, LIT MAN
                                                                                                                                   TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0
Matches 25; Conservative
NUMBER OF SEQ ID NOS: 2476
SOFTWARE: Patentin ver. 3.2
SEQ ID NO 2471
LENGTH: 25
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US-10-808-187-11
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APPLICANT: Gillim-Ross, Laura
APPLICANT: Gillim-Ross, Laura
APPLICANT: Gillim-Ross, Laura
APPLICANT: Taylor, Jil
APPLICANT: Scholl, David R.
APPLICANT: Scholl, David E.
APPLICANT: Wentworth, David E.
APPLICANT: Gillick, Joseph D.
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
TITLE OF INVENTION: Syndrome Coronavirus
FILE REFERENCE: DHI-07986
CURRENT APPLICATION NUMBER: US/10/699,936
CURRENT FILING DATE: 2003-11-03
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn version 3.2
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; Sequence 5, Application US/10889447
; Publication No. US2005007530741
; GENERAL INFORMATION:
    APPLICANT: Bennett, C. Frank
    APPLICANT: Bain, Ravi
    TITLE OF INVENTION:
    FILE REFERENCE: RTS-0685US
    CURRENT FILING DATE: 2004-07-12
    PRIOR PILICATION NUMBER: US/10/889,447
; CURRENT FILING DATE: 2003-07-12
; RILING DATE: 2003-07-12
; NUMBER OF SEQ ID NOS: 241
; SSETURE FALLSE (for Windows Version 4.0
; SEQ ID NO 5:
LENGTH: 28920
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100.0%; Score 25; DB 19;
Best Local Similarity 100.0%; Pred. No. 0.24;
Matches 25; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: SARS coronavirus Shanghai QXC
US-10-699-936-9
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ORGANISM: SARS coronavirus isolate BJ03
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; OTHER INFORMATION: n is any nucleotide US-10-889-447-5
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PRIOR FILING DATE: 2003-07-12
NUMBER OF SEQ ID NOS: 241
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                      SEQ ID NO 7
LENGTH: 29430
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LENGTH: 29727
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Publication No. US20050075307A1
GENERAL INFORMATION:
TGENERAL INFORMATION:
TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
FILE REFERENCE: RTS-0685US
CURRENT FILING DATE: 2004-07-12
PRIOR PLICATION NUMBER: 60486,670
PRIOR FILING DATE: 2003-07-12
NUMBER OF SEQ ID NOS: 241
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 0.24;
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TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION CURRENT APPLICATION MOBER: US/10/889,447
CURRENT FILING DATE: 2004-07-12
PRIOR APPLICATION NUMBER: 60/486,670
PRIOR APPLICATION NUMBER: 60/486,670
WINNER OF SEQ ID NOS: 241
SOFTWARE: FASTESQ 10 WINDOWS Version 4.0
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TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
FILE REPERENCE: RTS-0685US
CURRENT APPLICATION NUMBER: US/10/889,447
CURRENT FILING DATE: 2004-07-12
PRIOR APPLICATION NUMBER: 60/486,670
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100.0%; Score 25; DB
Best Local Similarity 100.0%; Pred. No. 0.2
Matches 25; Conservative 0; Mismatches
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Publication No. US20050075307A1
GENERAL INFORMATION:
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APPLICANT: Jain, Ravi
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Best Local Similarity 100.0
Matches 25, Conservative
                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
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NAME/KEY: misc_feature
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LENGTH: 28920
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APPLICANT: Comper, Wayne TITLE OF INVENTION: Charged Polysaccharides Resistant To Lysosomal Degradation Durin TITLE OF INVENTION: Kidney Filtration And Renal Passage And Their Use To Treat Or TITLE OF INVENTION: Prevent Infection By Coronaviruses
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TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: BLODANK. 013A
CURRENT APPLICATION NUMBER: US/10/839,729
CURRENT FILING DATE: 2004-05-04
PRIOR APPLICATION NUMBER: 60/468703
PRIOR APPLICATION NUMBER: 60/468703
PRIOR FILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 29727
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; ORGANISM: SARS-related coronavirus (Urbani strain)
US-10-827-757-1
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CURRENT APPLICATION NUMBER: US/10/827,757
CURRENT FILING DATE: 2004-04-20
PRIOR APPLICATION NUMBER: 60/464,294
PRIOR FILING DATE: 2003-04-21
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.2
TYPE: DNA
ORGANISM: SARS coronavirus isolate GZ01
                                                              NAME/KEY: misc_feature
LOCATION:
COTHER INFORMATION: n is any nucleotide
US-10-889-447-7
                                                                                                                                                                                                                                                                                                   1 CAGAACGCTGTAGCTTCAAAAATCT 25
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; Publication No. US20050002953A1
; GENERAL INFORMATION:
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US-10-839-729-15
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Best Local Similarity luv...
Local Similarity luv...
25; Conservative
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APPLICANT: Scholl, David R.
APPLICANT: Wentworth, David E.
APPLICANT: Wentworth, David E.
APPLICANT: Joillack, Ososph D.
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
TITLE OF INVENTION: Syndrome Coronavirus
TITLE REFERENCE: DHI.07986
CURRENT APPLICATION NUMBER: US/10/699,936
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Sequence 9, Application US/10889447

Publication No. US2050075307A1

APPLICANT: Bennett, C. Frank

APPLICANT: Bennett, C. Frank

TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION

FILE REFERENCE: RTS-0685US

CURRENT FILING DATE: 2004-07-12

PRIOR APPLICATION NUMBER: 05/486,670

PRIOR APPLICATION NUMBER: 60/486,670

PRIOR APPLICATION NUMBER: 2010-07-12

NUMBER OF SEQ ID NOS: 241

SOFTWARE: FREASEQ FOR Windows Version 4.0
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                                                                                APPLICANT: Jens Herold
TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
TITLE OF INVENTION: AND METHODS OF USE
FILE REPRENCE: BLODANK. 013A
CURRENT FILING DATE: 2004-05-04
PRIOR APPLICATION NUMBER: G/468703
PRIOR APPLICATION NUMBER: 60/468703
PRIOR APPLICATION NUMBER: 2003-05-06
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 29736
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Pred. No. 0.25;
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                Sequence 17, Application US/10839729
Publication No. US20050002953A1
GENERAL INFORMATION:
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CRGANISM: SARS coronavirus CUHK-W1
US-10-889-447-9
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; Publication No. US20050095582A1
; GENERAL INFORMATION:
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Best Local Similarity 100.0%;
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APPLICANT: Taylor, Jill
APPLICANT: Scholl, David R.
                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: SARS Coronavirus
US-10-839-729-17
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LENGTH: 29736
US-10-839-729-17
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Sequence 1, Application US/10699336

Publication No. US20050095582A1

GENERAL INFORMATION:

APPLICANT Gillim-Ross, Laura

APPLICANT Havior, Jill

APPLICANT Wentworth, David R.

APPLICANT Wentworth, David E.

APPLICANT Wentworth, David E.

TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory

TITLE OF INVENTION: Syndrome Coronavirus

FILE REFERENCE: DHI-07986

CURRENT APPLICATION NUMBER: US/10/699,936

CURRENT APPLICATION NUMBER: US/10/699,936

SOFTWARE: Patentin version 3.2

SEQ ID NOS: 87

SOFTWARE: Patentin version 3.2
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                                                                      Gaps
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Publication No. US20050075307A1

GENERAL INFORMATION:

APPLICANT: Bennett, C. Frank

APPLICANT: Jain, Ravi

TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION

FILE REFERENCE: RTS-068808

CURRENT APPLICATION NUMBER: US/10/889,447

CURRENT FILING DATE: 2004-07-12

PRIOR FILING DATE: 2003-07-12

NUMBER OF SEQ ID NOS: 241

SEQ ID NO 8

LENGTH: 29727
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Pred. No. 0.25;
                        DB 18; Length 29727;
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                        Query Match 100.0%; Score 25; DB 18
Best Local Similarity 100.0%; Pred. No. 0.25;
Matches 25; Conservative 0; Mismatches
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US-10-889-447-8
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; ORGANISM: SARS coronavirus Urbani
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## CREENT FILING DATE: 2003-11-03

## CROWNARS PatentIn Version 3.2

## SOCTUMARS: PatentIn Version 3.2

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## SOCTUMARS: PatentIn Version 3.2

## PatentIn Version 3.2

## ORGANISM: SAR8 coronavirus CUHK-W1

## ORGANISM: SAR8 coronavirus CUHK-W1

## CAPPARS: DNA

## CAPPARS: PatentING DATE: 2004-06-04

## PRIOR FILING DATE: 2004-06-04

## PRIOR FILING DATE: 2004-06-04

## PRIOR FILING DATE: 2004-06-04

## CAPPARS: PatentING DATE: 2004-06-04

## CAPPAR
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Search completed: May 16, 2005, 14:33:44 Job time : 1187.16 secs

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Scoring table:

Searched:

Database

Perfect score:

Run on:

Sequence:

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BZ381548 SALK 1168
BZ381547 SALK 1168
BZ381602 SALK 1169
AI662572 ma87903.x
CEN16811 K-EST0161
BY375756 BY375756
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

I (bases 1 to 826)

Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.

Wholbished (2001)

Other GSSs: BOHMB53TF

Contact: Chris Town
                                                                                                                                                         CE774308 tigr-gss-
                                                                                                                                                                                      AW213684 u090c05.x
AQ278670 CITBI-E1-
                                                                                                                                                                                                                                                                            BHS03697 80HM Brassica oleracea genomic clone BOHMB53, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:3712"
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CUS91647 P
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CB09888 b
CB09928 C
CB099218 b
CN206425 P
CC798330 c
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pred. No. 1.6e+02;
0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by Tom Osborn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 301-838-3523
Fax: 301-838-0208
Email: cdcown@rigr.org
DNA is from a doubled haploid provided |
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Brassica oleracea"
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BZ381548
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BZ381602
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CB116811
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337.038 Million cell updates/sec
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AI503985 A
AI503985 A
AO808522 I
AZ734853 I
BH754375 I
BJ71545 B
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BJ71545 B
BH728629 I
BH428629 I
BH51107 C
CA459517 A
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         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
                                             OM nucleic - nucleic search, using sw model
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AQ808522
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AI604651 BH428629

No. υ BJ718255

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 398)

88 Mahairas,G.G., Zackrone,K.D., Smith,T., Tipton,S., Schmidt,S.,

Traicoff,R., Abajian,C., Blanchard,A., West,A. and Hood,L.E.
Construction of a Characterized Clone Resource for Genomic
Sequencing: Generation and Preliminary Analysis of 20,000 Sequence
Tagged Connectors

N. Unpublished (1997)
Contact: Mahairas GG, Zackrone KD, Hood L
University of Washington
Seattle, WA 98195, USA
Tel: (206) 685-7301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BOIDSBITP BO 1.4_1.6_KB nuc Brassica oleracea genomic clone
BOIDSBI, genomic survey sequence.
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Brassica oleracea
Eukaryota, Viridplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="CIT Human Genomic Sperm Library C"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
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Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea (Unpublished (2001)
Other GSSs: BOIDS81TR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.2%; Score 18.8; DB 8; Length 398; 90.9%; Pred. No. 6.8e+02; ive 0; Mismatches 2; Indels
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DNA is from a doubled haploid provided by Tom Osborn.
Grap primer: TF
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_trye="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 398.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                      Email: kzackron@u.washington.edu
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Fax: 301-838-0208
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Bulk tissue was collected from a whole adult individual
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cloned into the Not I and EcoRV sites of pExpress-1.
Library was size-selected for >1 kb fragments. A
normalized version of this library is also available
(NHH ZGC 7). Library was constructed by Open Biosystems
(Huntsville, AL)."
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                                                                                                                                                                                                                                                                                                                                                                                                                          unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Genomics
National Cancer Genomics
National Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbb-remail.nih.gov
Tissue Procurement: Len Zon, Harvard
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llh.gov
Plate: LLAM14696 row: d column: 08
High quality sequence stop: 679.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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1 (bases 1 to 759)
11 (bases 1 to 759)
12 (bases 1 to 769)
13 (bases 1 to 769)
14 (bases 1 to 769)
15 (bases 1 to 769)
16 (bases 1 to 769)
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HS-1025-A1-D08-MF.abi CIT Human Genomic Sperm Library C Homo
sapiens genomic clone Plate=CT 804 Col=15 Row=G, genomic survey
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/clone="IMAGE:700298"
/tissue_type="whole body"
/lab_host="DH108"
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                                                                                                                                                                                  CF347362.1 GI:33790161
                                                                                                                                                                                                                            Danio rerio (zebrafish)
Danio rerio
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                                                                                                                       5', mRNA sequence.
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BM121685

184 bp mRNA linear EST 09-JUN-2003
L0500D10-3 NIA Mouse Newborn Heart cDNA Library Mus musculus cDNA
clone L0500D10 3', mRNA sequence.
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Piao,Y., Ko,N.T., Lim,M.K. and Ko,M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                      The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
                                                                                                                                                                                                             Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /lab host="E. coli DH10B"
/clone lib="ZMMBBb (HindIII)"
/note="Vector: pCUGI; Site_1: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                                                                          1 (bases 1 to 345)
Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C.,
Zohovetz, V., Fuke, G., Yu, Y., Wing, R. and Messing, J.
Sequencing of the maize genome at PGIR (2003c)
Unpublished (2003)
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Contact: Dawood B. Dudekula
Laboratory of Genetics
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                          CL239830 345 bp DNA linear GSK
ZMMBBb0576D01r ZMMBBb (HindIII) Zea mays genomic clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
191 Faz. 22 445 3801
Fax: 732 445 5735
Email: bhartii@waksman.rutgers.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                       ZMMBBb0576D01 3', genomic survey sequence
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/cultivar="B73"
/db_xref="taxon:4577"
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Location/Qualifiers
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Dr.Joachim Messing's lab
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BM121685.2 GI:31550974
                                                                                                                        CL239830.1 GI:40898081
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Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                         319 bp mRNA linear EST 20-JUN-2002
H4023F11-3 NIA Mouse 7.4K cDNA Clone Set Mus musculus cDNA clone
H4023F11 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cdna@lgsun.grc.nia.nih.gov
This clone set has been freely distributed to the community. Please
visit http://lgsun.grc.nia.nih.gov/cDNA/NIA_7_4k.html for details.
Plate: H4023 row: F collumn: 11
Seg primer: -21M13 Forward
High quality sequence stop: 319
POLYAA'se:
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VanBuren, V., Piao, Y., Dudekula, D.B., Qian, Y., Carter, M.G., Martin, P.R., Stagg, C.A., Bassey, U., Aiba, K., Hamatani, T., Kargul, G.J., Luo, A.G., Kelso, J., Hide, W. and Ko, M.S.H.
Assembly, verification, and initial annotation of NIA 7.4K mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone lib="NIA Mouse 7.4K cDNA Clone Set" /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; This clone is among a rearrayed set of 7,407 clones from more than 20 cDNA libraries."
/clone lib="BO 1.4 1.6 KB nuc"
/note="Vector: PHOS2; Site_1: BstXI; 1.4-1.6 kb sheared
nuclear DNA inserted into PHOS2 using BstXI linkers"
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Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA
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                                                                                                                        9; Length 611;
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                                                                                                                   Score 18.8; DB S
Pred. No. 7e+02;
0; Mismatches
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/db_xref="taxon:10090"
/clone="H4023F11"
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/organism="Mus musculus"
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/lab_host="DH10B"
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/strain="C57BL/6"
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Mus musculus
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BQ553690.1 GI:21454578
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larity 90.9%;
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                                                                                                                                                                                                                                                                                     /tissue_type="Newborn Heart"
/dev_stage="Newborn"
/dev_stage="Newborn"
/dev_stage="Newborn"
/dev_stage="Newborn"
/clone_lib="NIA Mouse Newborn Heart cDNA Library"
/note="Organ: heart; Vector: pSPORTI (Invitrogen); Site_1:
Sali, Site_2: Not1; Mouse cDNA project by the Laboratory
of Genetics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
Double-stranded cDNAs were synthesized with an Oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24.9 microgram of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The constant ligated to Lone-linker LL-Sal3 (Ref. Development 127:1173-1179 (2000) [PMID: 10725249]).

purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were digested with Sal1 and NorI enzymes, and cloned into Sal1 and NotI site of psPORTI plasmid vector. The DH10B E. coli host was the areasformed with ligation mixture by the chemical method. The average insert size is about 1.8 kb. The library was constructed by Yulan Piao (NIA)."
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333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
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The WashU-HMM Mouse BST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HMM Mouse EST Project
WashU-HMM Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74.4%; Score 18.6; DB 4; Length 384; 84.0%; Pred. No. 8.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Indels
                                                                                                                                                                                                                           db_xref="niaEST:L0500D10-3"
db_xref="taxon:10090"
clone="L0500D10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                   Email: cdna@lgsun.grc.nia.nih.gov
Plate: L0500 row: D column: 10
Seg primer: -21M13 Forward
High quality sequence stop: 384
POLYA*Yes.
                                                                                                                                                                   organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       358 CAGAACCCTCTAGCTCCAAAATAT 382
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                                                                                                                        Location/Qualifiers
                                                                                                                                                                                    /mol_type="mRNA"
/strain="C57BL/6J"
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AA771415.1 GI:2823226
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Best Local Similarity 84.09
Matches 21, Conservative
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AA771415/c
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JOURNAL
COMMENT
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AQ723105
HS 2083 A2 D09 MR CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2083 Col=18 Row=G, genomic survey
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases I to 453)
Mahalaras, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Eax: (206) 616-3887
Email: jwallace@u.washington.edu
Clonea may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:565398
Seg primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 406.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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/mol_type="genomic DNA"
                                                                                                                                                                          1. .414
/organism="Mus musculus"
                                                                                                                                                                                                                                               /db_xref="taxon:10090"
/clone="IMAGE:1001112"
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Location/Qualifiers
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Class: BAC ends
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AQ723105.1 GI:5482774
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Matches 21; Conserv
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'clone_lib="RIKEN full-length enriched, 17 days embryo
                                                                                                                                                    /dev_stage="17 days embryo"
/lab_host="DH10B"
                                                        /db xref="taxon:10090"
                                                                                                                                 tissue_type="head"
                                                                                 /clone="3322402N08"
     /mol_type="mRNA"
/strain="C57BL/6J"
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Best Local Similarity
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KEYWORDS
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Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
E. (Dasses I to 457)
S. Akimura, T., Arakawa, T., Carninci, P., Furuno, M., Hanagaki, T.,
Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Imotani, K.,
Ishi, Y., Ito, M., Kawai, J., Kojima, Y., Kouno, H., Kouda, M.,
Matsuyama, T., Nakamura, M., Nishi, K., Nomura, K., Numasaki, R.,
Okazaki, Y., Okido, T., Saito, R., Sakai, C., Sakai, K., Sakazume, N.,
Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T.,
Sogabe, Y., Suzuki, H., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Tanaka, T., Tomaru, A., Toya, T., Watahiki, A., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
RIKEN Encyclopedia of Mouse Full-length cDNAs (Akimura, T., et al.
                                                                                                                                                                                                                                                                .
0
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Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashiaxki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contect: Yoshlide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: genome-resegsc.riken.jp, URL:http://genome.gsc.riken.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new
wagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E.,
Matahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T.,
and Hayashizaki,Y.
                                                        /clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
                                                                                                                                                                                                                                                             Gaps
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0
                                                                                                                                                                                                             DB 8; Length 453;
                                                                                                                                                                                                                                                           Indels
Query Match

74.4%; Score 18.6; DB 8;
Best Local Similarity 84.0%; Pred. No. 8.5e+02;
Matches 21; Conservative 0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                      227 CAAAACACTTTAACTTCAAAAATCT 251
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                                                   /sex="mal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (2001)
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KEYWORDS
SOURCE
ORGANISM
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BB670372/c
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/organism="Mus musculus"

source

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was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 18.6; DB 2; Length 457;
Pred. No. 8.5e+02;
0; Mismatches 4; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seg primer: -28m13 rev2 ET from Amersham
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (1996)
Contact: Marra M/Mouse EST Project
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    High quality sequence stop: 394.
Location/Qualifiers
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Fax: 314 286 1810
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source
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PUBMED
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                                                                                                           AI503985 522 bp mRNA linear EST 11-WAR-1999 vm44e01.x1 Stratagene mouse diaphragm (#937303) Mus musculus cDNA clone IMAGE:1001112 3' similar to gb:L35933 Mouse erythrocyte protein 4.2 (MOUSE);, mRNA sequence.
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/tissue_type="diaphragm"
/dev stage="adult"
/lab_host="SOLK (kanamycin resistant)"
/clone lib="Stratagene mouse diaphragm (#937303)"
/note="Organ: diaphragm; Vector: pBluescript SK-; Site_1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. I (Bases I to 522)
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This clone was previously sequenced on the 5' end only, this new data is from the 3' end High quality sequence stop: 448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                  Length 459;
                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
                                                                                                                                                                                                                                                                                                                                                                Score 18.6; DB 1;
Pred. No. 8.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 366 cágaácccictágciccaaaatar 390
'db_xref="taxon:10090"
'clone="IMAGE:847202"
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 CAGAACGCTGTAGCTTCAAAAATCT 25
                                               /tissue_type="heart"
/dev_stage="4_weeks"
/lab_host="DH10B"
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AI503985.1 GI:4401836
                                                                                                                                                                                                                                                                                                                                                                ch 74.4%;
l Similarity 84.0%;
21; Conservative
                                     sex="male"
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Best Local Similarity
Matches 21; Conserv
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LOCUS
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KEYWORDS
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ORIGIN

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/clone lib="RPCI-11 Human Male BAC Library"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
BCORI, Site_2: XhoI; Cloned unidirectionally from mRNA
prepared from diaphragm muscle. Primer: Oligo dT. Average
insert size: 1.5 kb. Uni-ZAP XR Vector; -5' adaptor
sequence: 5' GAATTGGGCACGAG 3' ~3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTTTTTT 3'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AQ663564 1inear GSS 23-JUN-1999 HS 5476 A2 C09 T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1052 Col=18 Row=E, genomic survey sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 542)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618
Fax: (206) 616-3618
Fax: (206) 616-3887
Email: juallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.mad.buffalo.edu. Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
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                                                                                                                                                                                                                Length 522;
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                                                                                                                                                                                                                   Score 18.6; DB 1;
Pred. No. 8.6e+02;
0; Mismatches 4;
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High quality sequence stop: 542.
Location/Qualifiers
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/db_xref="taxon:9606"
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84.0%;
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Best Local (
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Search completed: May 16, 2005, 06:03:12
Job time : 2831.44 secs
                                            Mus musculus (house mouse)
Mus musculus
  AZ734853.1 GI:12500306
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
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Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3818
Emai: (206) 616-38187
Emai: jwallace@u washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
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(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
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1 (bases 1 to 545)
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
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Pred. No. 8.7e+02;
0; Mismatches 4; Indels (
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/db_xref="taxon:9606"
/clone="Plate=874 Col=18 Row=N"
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Location/Qualifiers
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  25
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Plate: 874 row: N column: 18
Seq primer: T7
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                          448 CAGGTCGCTGTAGATTCAAAAACT
1 CAGAACGCTGTAGCTTCAAAAATCT
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84.08;
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Matches 21; Conserv
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AQ808522
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AUTHORS
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/clone_lib="RPCI-24"
/note="Vector: pTARBAC1; Site_1: BamH1; Site_2: BamH1;
RPCI-24 Mouse BAC Library produced by Pieter de Jong. The
library was cloned in the pTARBAC1 cloning vector at the
BamH1 sites using MboI partially digested male CS7BL/6J
DNA."
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 673)
                                                                                                                                                                         Zhao, S., Nierman, W., Malek, J., Shatsman, S., Akinret, B., Levins Tsegaye, G., Geer, K., Krol, M., Shvartsbeyn, A., Gebregeorgis, E., Russell, D., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-24
Unpublished (1999)
Other GSSs: RPCI-24-120P3.TJ
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SQGSEYDYVIFTQTTETAHSCNVNRFNVAITRAKIGILCIMSDRDLYD"
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SARS coronavirus TW-HP1
Viruses, saRNA positive-strand viruses, no DNA stage, Nidovirales,
Coronaviridae, Coronavirus.

1 (bases 1 to 626)
Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J.,
Molecular Epidemiology of SARS in Taiwan - Development of a Simple
Method for Tracing the Origin and Dissemination of SARS

Virus C. (bases 1 to 626)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J., Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M.-Arthur.

Direct Submission
Submitted (28-0CT-2003) National Yang-Ming University, AIDS
Prevention and Research Center, 155, Li-Nong St., Sec.2, Peitou, Taipei, Taiwan 112, R.O.C.

Location/Qualifiers
  SARS
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SARS coronavirus TW-HP1 isolate TW-HP1_SC18 replicase 1B gene,
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SARS coronavirus TW-HP2

Viruses, seRNA positive-strand viruses, no DNA stage; Nidovirales;
Viruses; seRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.

I (bases 1 to 626)

SS Lan,Y.-C., Chen,Y.-Y. and Chen,Y.-M.Arthur.

Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS

Lupublished

SS Lan,Y.-C., Chen,Y.-Y. and Chen,Y.-M. Liu,T.-T., Lu,J.-J., Chan,Y.-J.,
Yang,J.-Y., Chen,H.-Y. and Chen,Y.-M.Arthur.

Direct Submission

AL Submitted (28-COT-2003) National Yang-Ming University, AIDS

Prevention and Research Center, 155, Li-Nong St., Sec.2, Peitou,
Taipei, Taiwan 112, R.O.C.

Location/Qualifiers
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SARS coronavirus TW-HP3
SARS coronavirus TW-HP3
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
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kS Lan,Y.-C., Chen,Y.-J., Lee,C.-M., Liu,T.-T., Lu,J.-J., Chan,Y.-J.,
Yang,J.-Y., Chen,H.-Y. and Chen,Y.-M.Arthur.
Molecular Epidemiology of SARS in Taiwan - Development of a Simple
Method for Tracing the Origin and Dissemination of SARS
LD Upublished
E (bases 1 to 626)

KS Lan,Y.-C., Chen,H.-Y. and Chen,Y.-M. Liu,T.-T., Lu,J.-J., Chan,Y.-J.,
Yang,J.-Y., Chen,H.-Y. and Chen,Y.-M.Arthur.
Direct Submission
North Submitted (28-OCT-2003) National Yang-Ming University, AIDS
Prevention and Research Center, 155, Li-Nong St., Sec.2, Peitou,
Taipei, Taiwan 112, R.O.C.
Taipei, Taiwan 112, R.O.C.
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Taipei, Taiwan 112, R.O.C.
Arguellifiers
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Viruses, saRNA positive-strand viruses, no DNA stage, Nidovirales,
Viruses, SaRNA positive-strand viruses, no DNA stage, Nidovirales,
Coronaviridae, Coronavirus.

1 (bases 1 to 626)
Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J.,
Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M. Arthur.
Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS
Unpubbished
2 (bases 1 to 626)
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Direct Submission
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SARS coronavirus TW-HP4 isolate TW-HP4_SC18 replicase 1B gene,
partial cds.
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AY451932/c

RESULT 5

Matches

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ORIGIN

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ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS

REFERENCE AUTHORS

JOURNAL

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                                                                                       Viruses; SSRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.

1 (Dases 1 to 626)
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Lan,Y.-C., Chen,Y.-J., Lee,C.-M., Liu,T.-T., Lu,J.-J., Chan,Y.-J.,
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2 (bases 1 to 626)
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Location/Qualifiers
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1 (bases 1 to 626)
Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J., Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M.Arthur.

Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS
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SARS coronavirus TW-JC2
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.

1 (bases 1 to 626)
Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J.,
Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M. Arthur.
Melecular Epidemiology of SARS in Taiwan - Development of a Simple
Method for Tracing the Origin and Dissemination of SARS
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lan, Y.-C., Chon, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J., Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M.Arthur.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (28-OCT-2003) National Yang-Ming University, AIDS
Prevention and Research Center, 155, Li-Nong St., Sec.2, Peitou,
                                                                                                                                                                                                                                                                                                                                                                                                           AY51932 626 bp RNA linear VRL 28-FEB
SARS coronavirus TW-JC2 isolate TW-JC2_SC18 replicase 1B gene,
partial cds.
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/mol_type="genomic RNA"
/isolate="TW-JC2_SC18"
/db_xref="taxon:264375"
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Location/Qualifiers
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EYFNSVCRLMKTIGPDMFLGTCRRCPAEIVDTVSALVYDNKLKAHKDKSAQCFKMFYK
GVITHDVSSAINRPQIGVVREFLTRNPAWRKAVFISPYNSQNAVASKILGLPTGTVDS
SQGSEYDYVIFTQTTETAHSCNVNRFNVAITRAKIGILCIMSDRDLYD"
                                          SARS coronavirus TW-GD2 isolate TW-GD2_SC18 replicase 1B gene, partial cds.
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protein_id="AAS44822.1"
|db_xref="GI:42741345"
|translation="ISMATNYDLSVVNARLRAKHYVYIGDPAQLPAPRTLLTKGTLEP
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1 (Bases I to 626)

1 (Bases I to 6.2)

1 (Bases I to 6.2)

Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M. Arthur.

Molecular Epidemiology of SARS in Taiwan - Development of a Simple without for Tracing the Origin and Dissemination of SARS

Unpublished

2 (Bases I to 626)

2 (Bases I to 6.2)

2 (Bases I to 6.2)

Yang, J.-Y., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J., Yang, J.-Y., Chen, Y.-J., Arthur.
                                                                                                                                                                                                                   SARS coronavirus TW-GDZ
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.

(Conses 1 to 626)
Lan,Y.-C., Chen,Y.-J., Lee,C.-M., Liu,T.-T., Lu,J.-J., Chan,Y.-J.,
Yang,J.-Y., Chen,H.-Y. and Chen,Y.-M.Arthur.
Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lu, J.-J., Chan, Y.-J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Lan,Y.-C., Chen,Y.-J., Lee,C.-M., Liu,T.-T., Lu,J.-J., Chan,Y.-J
Yang,J.-Y., Chen,H.-Y. and Chen,Y.-M.Arthur.
Direct Submission
Submitted (28-6CT-2003) National Yang-Ming University, AIDS
Prevention and Research Center, 155, Li-Nong St., Sec.2, Peitou,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 626;
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/mol type="genomic RNA"
/isolate="TW-GD2_SC18"
/db_xref="taxon:264379"
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Location/Qualifiers
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AY451937.1 GI:42741346
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SARS coronavirus TW-GD3
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Best Local Similarity 100.
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AY451936/c
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EXFNSVCRIMKTIGPDWRLGTCRRCPABIVDTVASALVYDNKARHKDKSAQCFKWFYK
GVITHDVSSAINRPQIGVREFLTRPAMKKAVFISPYNSQNAVASKILGLFTQTVDS
SQGSEZDYVIFTQTTETAHSCRNNRFNVAITRAKIGILCIMSDRDLYD"
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GVITHDVSSAINRPQIGVVREPLTRNPAWRKAVFISPYNSQNAVASKILGLPTQTVDS
SQGSEYDYVIFTQTTETAHSCNVNRFNVALTRAKIGILCIMSDRDLYD"
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1 (bases 1 to 626)
Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J., Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M. Arthur.

Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS
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Direct Submission
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Pred. No. 0.48;
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Pred. No. 0.48;
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/mol_type="genomic RNA"
/isolate="TW-GD1_SC18"
/db_xref="taxon:264378"
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                                                                                       /codon_start=1
/product="replicase 1B"
/protein_id="AAS44820.1"
/db_xref="GI:42741341"
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/protein_id="AAS44821.1"
/db_xref="G1:42741343"
/mol_type="genomic_RNA"
/isolate="TW-KC3_SC18"
/db_xref="taxon:264377"
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Best Local Similarity 100.0%;

Matches 25; Conservative 0;
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SARS coronavirus TW-GD1
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Best Local Similarity 100.0%;

Matches 25; Conservative 0,
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AY451935/c
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SARS coronavirus TW-GD5 isolate
partial cds.
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SARS coronavirus TW-YM1
partial cds.
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SARS coronavirus TW-YM1
       100.08;
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2 (bases 1 to 626)
                             25; Conservative
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GVITHDVSSAINRPQIGVVREFLTRNPAMRKAVFISPYNSQNAVASKLIGLPTGTVDS
SQGSEYDYVIFTGTTETAHSCNVNRFNVAITRAKIGILCIMSDRDLYD"
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GVITHDVSSAINRPQIGVVREFLTRNPAMRKAVFISPYNSQNAVASKILGLPTQTVDS
SQGSEYDYVIFTQTTETAHSCNVNRFNVAITRAKIGILCIMSDRDLYD"
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Yang,J.-Y., Chen,H.-Y. and Chen,Y.-M.Arthur.

Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS

Unpublished
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SARS coronavirus TW-GD4
SARS coronavirus TW-GD9
Viruses; SRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
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Direct Submission
Submitted (28-OCT-2003) National Yang-Ming University, AIDS
Prevention and Research Center, 155, Li-Nong St., Sec.2, Peitou,
Taipei, Taiwan 112, R.O.C.
Location/Qualifiers
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SARS coronavirus TW-GD4 isolate TW-GD4_SC18 replicase 1B gene,
partial cds.
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                                                                                                                /organism="SARS coronavirus TW-GD3"
Monl type="genomic RNA"
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100.0%; Pred. No. 0.48;
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                                                                                                                                                                                                         /codon_start=1
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DB 14; Length 626;

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Query Match

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<1. _ . > 626
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GVITHDVSSAINRPQIGVVREFLTRNPAWRKAVFISPYNSQNAVASKILGLPTQTVDS
SQGSEYDYVIFTQFTBTAHSCNVNRFNVAITRAKIGILCIMSDRDLYD"
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TW-GD5_SC18 replicase 1B gene,
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1 (bases 1 to 626)
Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J., Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M. Arthur.
Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS
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Direct Submission
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Prevention and Research Center, 155, Li-Nong St., Sec.2, Peitou, Taipei, Taiwan 112, No.C.
Location/Qualifiers
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1 (bases 1 to 626)
Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J.,
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/isolate="TW-GD5 5218"
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SQGSEZVYYFYQTFTTAHSCNVNRFFVNATTRAKIGILCIMSDRDLYD"
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1 (bases 1 to 626)
Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J., Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M. Arthur.

Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS
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[Lan,Y.-C., Chen,Y.-J., Lee,C.-M., Liu,T.-T., Lu,J.-J., Chan,Y.-J.,
Lan,Y.-C., Chen,Y.-J., and Chen,Y.-M.Arthur.

Direct Submission
Submitted (28-OCT-2003) National Yang-Ming University, AIDS
Prevention and Research Center, 155, Li-Nong St., Sec.2, Peitou, Taipei, Taiwan 112, R.O.C.

Location/Qualifiers
Yang,J.-Y., Chen,H.-Y. and Chen,Y.-M.Arthur.
Molecular Epidemiology of SARS in Taiwan - Development of a Simple
Method for Tracing the Origin and Dissemination of SARS
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SQGSEYDYVIFTQTTETAHSCNVNRFNVAITRAKIGILCIMSDRDLYD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALMASLY42 626 bp RNA linear VRL 28-FEB-2004 SARS coronavirus TW-YM3 isolate TW-YM3_SC18 replicase 1B gene, partial cds.
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/translation="ISMATNYDLSVVNARLRAKHYVYIGDPAQLPAPRTLLTKGTLEP
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Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronavirudae; Coronavirus.

Coronaviridae; Coronavirus.

1 (bases 1 to 626)
Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J., Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M.Arthur.

Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS
Unpublished

2 (bases 1 to 626)
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Direct Submission
Submitted (28-0CT-2003) National Yang-Ming University, AIDS
Prevention and Research Center, 155, Li-Nong St., Sec.2, Peitou, Taipei, Taiwan 112, R.O.C.

Location/Qualifiers
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/codon_start=1
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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May 15, 2005, 17:17:00 ; Search time 320.703 Seconds (without alignments) 461.466 Million cell updates/sec Run on:

US-10-808-187A-2472 25

Perfect score: Title:

1 tcagaaccctgtgatgaatcaacag 25 Sequence:

IDENTITY NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 seqs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

N Geneseq 16Dec04: geneseqn1980s:* 2: genesegn1990s:*

geneseqn2003cs:* geneseqn2003ds:* geneseqn2004as:* geneseqn2004bs:* geneseqn2002as:*geneseqn2002bs:* geneseqn2003as:* geneseqn2003bs:* geneseqn2000s:* geneseqn2001as:* geneseqn2001bs: 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Adj39000 SARS coro	Acc57972 Canola pr	Aax51917 Human sec	Adl12960 Human ste	Abz11767 Human pol	Adm44285 Novel hum	ytochrom	Human cDN	ın rep	tes	1 ste	can	can	ŭ ŭ	hum	hil	hi1	pol	DNA	sedn
	Acc	Aax51	Ad112	Abz11767	Adm44285	Aai66415 Cytochrom	Aah18169 Hur	Aal04982 Hume	Ab197875 Human tes	Adl12627 Human ste	Adq97061 Mouse car	Abd32866 Mouse car	Ada60091 Soybean p	Adq63113 Novel hum	Abl10352 Drosophi	Abl10338 Drosoph:	Aai82162 Human pol	Aas94803 Human	Acc61068 Gene
ADJ39000	ACC57972.	AAX51917	ADL12960	ABZ11767	ADM44285	AA166415	AAH18169	AAL04982	ABL97875	ADL12627	ADQ97061	ABD32866	ADA60091	ADQ63113	ABL10352	ABL10338	AAI82162	AAS94803	ACC61068
12	8	7	12	9	12	4	4	4	4	12	17	13	σ	12	4	4	4	φ	10
29751	2400	436	1067	1169	1169	2386	2950	4511	4511	5520	135462	192992	276	2716	3755	3986	394	1653	1689
100.0	75.2	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	74.4	72.8	72.8	72.8	72.8	72.0	72.0	71.2
25	18.8	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.6	18.2	18.2	18.2	18.2	18	18	17.8
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Adk62847 Disease t	Adk67447 Baker's y	Ad143131 Human ova	Aas34286 Human cDN	Aba58142 Human foe	Aba58678 Human foe	Aai38357 Probe #70	Aai37749 Probe #64	Aak32530 Human bon	Aak31881 Human bon	Aak06811 Human bra	Aak06222 Human bra	Abs32241 Human liv	Abs31570 Human liv	Abs06642 Human gen	Abs07319 Human gen	Adl36747 Human ova	Adi71591 Human ova	Adp04744 Sea squir	Aaz28369 Protein p	Abn68560 Streptoco	Aaa88551 Human dua	Continuation (17 o	Continuation (5 of	Continuation (6 of
ADK62847	ADK67447	ADL43131	AAS34286	ABA58142	ABA58678 .	AAI38357	AAI37749	AAK32530	AAK31881	AAK06811	AAK06222	ABS32241	ABS31570	ABS06642	ABS07319	ADL36747	ADI71591	ADP04744	AAZ28369	ABN68560	AAA88551	ABN71527 16	ABQ74964 ⁷ 4	ABQ74964 ⁻⁵
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17.8	17.8	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6	17.6
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ALIGNMENTS

RESULT 1

small interfering RNA; siRNA; modified ribonucleotide, viral replication inhibition; hepatitis C virus; HCV; hepatitis C; antiinflammatory; hepatotropic; virucide; hepatitis A virus; hepatitis D virus; hepatitis E virus; Ebola virus; influenza virus; rotavirus; reovirus; retrovirus; poliovirus; human papilloma virus; metapneumoniavirus; coronavirus; viral infection; gene; ds. SARS coronavirus nucleotide sequence. ADJ39000/c ID ADJ39000 standard; DNA; 29751 BP. (first entry) 06-MAY-2004 ADJ39000;

SARS coronavirus.

WO2004011647-A1.

05-FEB-2004.

25-JUL-2003; 2003WO-US023104.

26-JUL-2002; 2002US-0398605P

(CHIR) CHIRON CORP.

Seo MY, Houghton M; Han J,

WPI; 2004-143862/14.

New RNase resistant small interfering RNA, useful for treating viral infections, e.g., hepatitis C, influenza virus or coronavirus infection.

Example 10; Fig 3; 74pp; English.

The present invention describes a small interfering RNA (siRNA) which comprises a modified ribonucleotide, where the siRNA is resistant to RNase and retains the ability to inhibit viral replication. Also described: (1) inactivating a virus in a patient; (2) making a modified siRNA that targets a nucleic acid sequence, in a virus; (3) a double-

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Stranded RNA molecules of 10.30 indicatories characteries coward and the patities of virus (HCV); (4) indicing targeted RNA interference toward HCV in hepatic cells; (5) inhibiting replication of HCV; (6) a vector comprising DNA segment encoding the RNA molecule; (7) a host cells comprising the vector of (6); (8) inhibiting replication of HCV in cells carrying HCV; (9) treating hepatitis C in a subject; (10) a modified sirRNA molecule comprising a double-stranded RNA molecule of 10.30 corrying HCV; (9) treating hepatitis C in a subject; (10) a modified sirRNA molecules in length, which mediates RNA interference toward a target agent or virus and is linked to at least one receptor-binding ligand; and collection argued and virus for a least one receptor-binding ligand; and molecules have antihiflammatory, hepatotropic and viruside activities. The miditied RNA molecules are useful for inactivating virus in mammalian cells. The siRNAs are useful for treating hepatitis C virus, hepatitis D virus, hepatitis B virus, poliovirus, influenza virus, netapneumoniavirus or coronavirus inflections. The methods of the virus, metapneumoniavirus or coronavirus inflections. The methods of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New protein kinase stress-related polypeptide coding nucleic acid, useful for producing transgenic plants with an increased tolerance to an environmental stress, e.g. high salinity, as compared to a wild type
                                                                                                                                                                                                                                                                                                                                     invention can be used to correct or compensate for cellular physiological abnormalities involved in conferring susceptibility to viral infections in patients and/or alleviate symptoms of a viral infection in patients.
                                                                                                                                                                                                                                                                                                                                                                                                      sequence represents the SARS coronavirus nucleotide sequence
stranded RNA molecule of 10-30 nucleotides that inhibits replication of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BnPK-4; protein kinase stress-related polypeptide; PKSRP; enzyme; transgenic plant; plant; stress tolerance; drought tolerance; salt tolerance; cold tolerance; canola; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 29751 BP; 8478 A; 5941 C; 6188 G; 9144 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                          which is used in an example from the present invention.
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100.0%;
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Best Local Similarity luv...
Best 25; Conservative
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The present sequence is a full-length cDNA encoding BnPK-4, a novel canola protein kinase stress-related polypeptide (PKSRP). The CDNA was identified on the basis of homology to Physcomitrella patens PK-3 (see ACC57962) and PK-10 (see ACC57966) sequence. BnPK-4 is an example of PKSRPB of the invention that are important for modulating a plant's response to environmental stress. Over-expression of PKSRP coding nucleic acids in a plant results in the plant's increased tolerance to environmental stress. Transgenic monocot and dicot plants are provided that show increased tolerance to high salinity, drought and low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated brain-derived nucleic acids - used to develop products which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; secreted protein, EST; expressed sequence tag; diagnosis; forensic; gene therapy; chromosome mapping; signal peptide; upstream regulatory sequence; cyrokine activity; cell proliferation; differentiation; haematopoiesis regulation; tissue growth regulation; reproductive hormone regulation; chemocactic; chemokinetic; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AMX51787 to AAX52019 represent 5' expressed sequence tags (ESTB) for human secreted proteins, and encode the proteins given in AAY122987 to AAY13219, respectively. The proteins given represent the signal peptide and an N-terminal fragment of a secreted protein. The nucleic acid sequences can be used for producing secreted human gene products. They can also be used to develop products for diagnosis and therapy. The proteins obtained may have cytokine activity, cell proliferation/differentiation activity, haematopoiesis regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nay have cytokine, immune, regulatory, haematopoiesis regulating, anti-
inflammatory or tumour inhibition activity.
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                                                                                                                                                                                                                                                                                            Score 18.8; DB 8; Length 2400;
Pred. No. 1e+02;
); Mismatches 2; Indels 0
                                                                                                                                                                                                                                                          Sequence 2400 BP; 702 A; 511 C; 500 G; 687 T; 0 U; 0 Other;
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               Claim 1; Page 92-93; 111pp; English.
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90.9%;
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Best Local Similarity
Matches 20; Conserv
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AAX51917/c
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The invention relates to a combination comprising cDNAs that are differentially expressed in response to steroid treatment. Also included are the following: a high throughput method for using a cDNA to detect differential expression of nucleic acids in a sample; and a high throughput method of screening molecules or compounds to identify a ligand that specifically binds a cDNA. The sample is from a subject with Wilson disease and comparison of a standard defines a stage of that disease. The high throughput method of screening molecules or compounds to identify a ligand that specifically binds a cDNA comprises: combining the combination with molecules or compounds under conditions to allow specific binding; and detecting specific binding between each cDNA and least one molecule or compound. The molecules or compounds are regulatory proteins. The combination is useful for preparing a composition for treating liver disorders associated with steroid therapy, e.g., cirrhosis or hepaticits. The present sequence represents a human cDNA which is differentially expressed in steroid-induced C3A liver cells. Note: The
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activity, tissue growth regulating activity, reproductive hormone regulating activity, chemotactic/ chemokinetic activity, haemostatic and thrombolytic activity, receptor/ ligand activity, anti-inflammatory activity, tumour inhibition activity or other activities. The products can be used in forensic, gene therapy and chromosome mapping procedures. The sequences can also be used for obtaining corresponding promoter sequences. The nucleic acids encoding the signal peptide can be used for directing extracellular secretion of a polypeptide or the insertion of a polypeptide into a membrane, or importing a polypeptide into a cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Combination useful for preparing a composition for treating liver disorders associated with steroid therapy, e.g., cirrhosis or hepatitis, comprises cDNAs that are differentially expressed in response to steroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ss; gene; Hepatotropic; Gene therapy; Wilson disease; liver disorder; steroid therapy; cirrhosis; hepatitis; human; C3A liver cell.
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                                                                                                                                                                                                                 Sequence 436 BP; 111.A; 80 C; 109 G; 132 T; 0 U; 4 Other;
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                                                                                                                                                                                                                                     74.4%; Score 18.6; I
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0; Mismatches
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les 21; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; genome mapping; gene therapy; food supplement; virus; fungus; cell-proliferative disorder; neurodegenerative disease; bacterial; Parkinson's disease; Alzheimer's disease; autoimmune disease; multiple sclerosis; diabetes; genetic disorder; wound; burn; infection; arthritis; cytostatic; immunomodulator; nootropic; neuroprotective; antiparkinsonian; antidabetic; immunosuppressive; dermatological; haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide; antiarthritic; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polynucleotides comprising sequences assembled from expressed sequence tags (ESTs), useful for treating cell-proliferative, neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.
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Ghosh M;
                                                                                                                   / Match 74.4%; Score 18.6; DB 12; Length 1067; Local Similarity 84.0%; Pred. No. 1.1e+02; hes .21; Conservative 0; Mismatches 4; Indels 0;
                                                                                   Sequence 1067 BP; 291 A; 220 C; 196 G; 355 T; 0 U; 5 Other;
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Ma Y, Yamazaki V, Chen R, Wang Z,
J, Wang D, Drmanac RT;
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Xue AJ, Yang Y, Ma
Wehrman T, Wang J,
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04-DEC-2001
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arthritis, etc. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene; human; arginine-rich protein; cancer; inflammation;
                                                                                                      Sequence 1169 BP; 361 A; 198 C; 254 G; 356 T; 0 U; 0 Other;
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                                                                                                                                                   Query Match 74.4%; Score 18.6; DB 6; Best Local Similarity 84.0%; Pred. No. 1.1e+02; Matches 21; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human arginine-rich protein cDNA #649
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                                                                                                                                                                                                                                                                                    213 TCAGAACCATGGGATGTATCAGCAG 189
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ADM44285 standard; cDNA; 1169
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05-MAR-2002; 2002WO-US005095.
20-AUG-2002; 2002US-00225251.
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(XUEA/) XUE A.
(DRMA/) DRMANAC R T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genetic disorder
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The present invention provides the protein and coding sequences of cytochrome C oxidase CO11 rptoein 9. The sequences can be used in the treatment of cancer and HIV infection. The present sequence is the coding
                                                                                                                                                          Cytochrome C oxidase CO11 protein 9; cancer; HIV infection; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polypeptide-cytochrome C oxidase COII protein 9 and polynucleotide for coding this polypeptide.
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                                                                                                                          Cytochrome C oxidase CO11 protein 9 coding sequence.
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Pred. No. 1.3e+02;
0; Mismatches 4;
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                    BP.
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AA166415/c
ID AA166415 standard; cDNA; 2386
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84.0%;
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Best Local Similarity 84.vv
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213 TCAGAACCATGGGATGTATCAGCAG 189

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1 TCAGAACCCTGTGATGAATCAACAG 25

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2000US-0231243P.
2000US-0231244P.
2000US-0231413P.
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2000US-0232080P.
2000US-0232081P.
2000US-0231968P.
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2000US-0234223P.
2000US-0234274P.
2000US-0234997P.
                                                                                         16-MAR-2000; 2000US-0189874P.
17-MAR-2000; 2000US-0190076P.
18-APR-2000; 2000US-0198123P.
                                                                                                                                    19-MAY-2000; 2000US-0205515P.
07-UUN-2000; 2000US-0209467P.
28-UUN-2000; 2000US-021486FP.
30-JUN-2000; 2000US-0215135P.
07-JUL-2000; 2000US-0216647P.
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14-JUL-2000; 2000US-0218290P.
26-JUL-2000; 2000US-0220963P.
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26-JUL-2000; 2000US-0220964P.
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14-AUG-2000; 2000US-0224519P.
14-AUG-2000; 2000US-0225213P.
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2000US-0232398P.
2000US-0232399P.
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2000US-0233063P.
2000US-0233064P.
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14-AUG-2000; 2000US-0225268P.
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2000US-0229287P.
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2000US-0229509P.
    17-JAN-2001; 2001WO-US001339
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2000US-0225757P
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2000US-0235484P
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2000US-0236367P
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18-AUG-2000;
22-AUG-2000;
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12-SEP-2000;
14-SEP-2000;
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14-SEP-2000;
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08-SEP-2000;
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25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
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05-SEP-2000;
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    lime present interaction describes primer sets for synthesisting by sold in the present interaction describes primer sets for synthesisting sold in the specification. Where a primer set comprises:

(a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the S602 nucleotide sequences defined in the specification, where the of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 3'-end sequence and an oligonucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence, where the oligonucleotide comprises a 1'-end sequence, where the oligonucleotide comprises a 1'-end sequence, where the oligonucleotide comprises a 1'-end sequence complementary to a program of the 5'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primer sets allow obtaining of the full-length cDMAs. The primers are also useful for the full-length cDMAs. The primers allow obtaining of the full-length cDMAs. The primers allow obtaining of the full-length cDMAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13623 represent human amino acid sequences; and AAH13629 to AAH13632 represent coligonucleotides, all of which are used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                             Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; reproductive system related antigen; reproductive system disorder;
                                                                                                                                                                                                                                                                                                        The present invention describes primer sets for synthesising 5602 full-
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                                                                                                                       Yamamoto J;
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                                                                                                                                                                                                                                                                     Claim 8; SEQ ID NO 18065; 2537pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2950 BP; 840 A; 578 C; 587 G; 945 T; 0 U; 0 Other;
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                                                                                                                    Saito K, Ye, Otsuki T;
                                                                                                                      Hayashi K, S
A, Nagai K,
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                                                                                                                                    Sugiyama T, Wakamatsu
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29-JUL-1999; 99JP-00248036.
27-ANG-1999; 99JP-00300253.
11-JAN-2000; 2000JP-00118776.
02-MAY-2000; 2000JP-00183767.
09-JUN-2000; 2000JP-002418999.
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Best Local Similarity 84.0%
....hes 21; Conservative
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                                                                                        (HELI-) HELIX RES INST.
                                                                                                                                                                  WPI; 2001-318749/34.
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                                                                                                                      Ota T,
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Gaps

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Length 4511;

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The present invention provides the protein and coding sequences of a number of human reproductive system related antigens. These can be used in the prevention and treatment of reproductive system disorders, including cancer. The present sequence is a genomic sequence encoding a protein of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; testicular antigen; testes; cancer; metastasis; immune disorder; reproductive system disorder; pene therapy; cardiovascular disorder; respiratory disorder; neurological disorder; gastrointestinal disease; infection; cytostatic; gene; ds.
used in preventing, treating or ameliorating a medical condition
                                    Disclosure; SEQ ID NO 7670; 1297pp + Sequence Listing; English.
                                                                                                                                                                                     Sequence 4511 BP; 1177 A; 1009 C; 1055 G; 1270 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human testicular antigen encoding DNA fragment SEQ ID NO: 2527,
                                                                                                                                                                                                                      Score 18.6; DB 4;
Pred. No. 1.4e+02;
0; Mismatches 4;
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2000US-0198123P.
2000US-0205515P.
2000US-0219486FP.
2000US-0214886P.
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2000US-0225447P.
2000US-0225757P.
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                                                                                                                                                                                                                                                            21; Conservative
                                                                                                                                                                                                                                           Local Similarity
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14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
14-AUG-2000;
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24-FEB-2000;
02-MAR-2000;
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28-JUN-2000;
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2000US - 0241809P

2000US - 0246474P

2000US - 0246524P

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2000US - 0246521P

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2000US - 024651P

2000US - 024651P

2000US - 024621P

2000US - 024920P

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2000US-0250.391P.
2000US-0251.30P.
2000US-0251.98P.
2000US-0251.479P.
2000US-0251.86P.
2000US-0251.86P.
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2000US-0237039P
2000US-0239935P
2000US-0239935P
2000US-024123P
2000US-0241221P
2000US-0241786F
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20-OCT-2000;
01-NOV-2000;
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08-NOV-2000;
                    NOV-2000
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The present invention provides the protein and coding sequences of 973 human testicular antigens, and fragments of their genomic sequences. The sequences can be used in the treatment of cardiovascular, urinary system, reproductive system, immune, respiratory, neurological and gastrointestinal disorders, infections, and particularly cancer, especially testicular cancers. The present sequence is a DNA encoding a protein fragment of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding 973 human testicular antigen polypeptides, useful for preventing, diagnosing and/or treating testicular cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 2527; 766pp; English
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ID ADL12627 standard; cDNA; 5520 BP.
XX
AC ADL12627;
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17-NOV-2000; 2000US-0249300P
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06-DEC-2000; 2000US-0251479P
08-DEC-2000; 2000US-0251856P
                                                                                                                                                                                                                                                                                                                                                                                                                                                       (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-483232/52.
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Best Local Similarity
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Gaps

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New isolated cancer associated nucleic acids comprising at least 10 contiguous nucleotides, useful for diagnosing, preventing and/or treating cancers such as leukemia and lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to cancer associated sequences (ADQ97025-ADQ98004). The sequences are useful for the diagnosis, prevention and/or treatment of cancer, such as leukemia and lymphoma. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formate directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 135462 BP; 34707 A; 29305 C; 31635 G; 39360 T; 0 U; 455 Other;
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Pred. No. 2.4e+02;
0; Mismatches 4;
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14-WAR-2003; 2003US-00388838.
15-APR-2003; 2003US-00417375.
13-JUN-2003; 2003US-00461862.
15-SEP-2003; 2003US-00663431.
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                                                                                                                                  27-DEC-2002; 2002US-00330773.
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84.0%;
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Query Match

Best Local Similarity 84.00,

Thes 21; Conservative
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13-JUN-2003;
15-SEP-2003;
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                                            22-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a combination comprising cDNAs that are differentially expressed in response to steroid treatment. Also included are the following: a high throughput method for using a cDNA to detect differential expression of nucleic acids in a sample; and a high throughput method of screening molecules or compounds to identify a ligand that specifically binds a cDNA. The sample is from a subject with Wilson disease and comparison of a standard defines a stage of that disease. The high throughput method of screening molecules or compounds to identify a ligand that specifically binds a cDNA comprises; combining the combination with molecules or compounds under conditions to allow specific binding; and detecting specific binding between each cDNA and at section or compound. The molecules or compounds are regulatory proteins. The combination is useful for preparing a composition for treating liver disorders associated with steroid therapy, e.g., cirrhosis or hepatitis. The present sequence represents a human cDNA which is differentially expressed in steroid-induced CSA liver cells. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Combination useful for preparing a composition for treating liver disorders associated with steroid therapy, e.g., cirrhosis or hepatitis, comprises cDNAs that are differentially expressed in response to steroid treatment.
                                          ss; gene; Hepatotropic, Gene therapy, Wilson disease; liver disorder; steroid therapy; cirrhosis; hepatitis; human; C3A liver cell.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 74.4%; Score 18.6; DB 12; Best Local Similarity 84.0%; Pred. No. 1.4e+02; Matches 21; Conservative 0; Mismatches 4;
Human steroid-induced C3A liver cell cDNA #356.
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AD097061;

RESULT 12 ADQ97061/

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The invention relates to an isolated nucleic acid comprising at least 10 contiguous nucleotides of any of the 233 polynucleotide sequences given in the specification, or its complement. The nucleic acids encode cancerassociated proteins. Also included are an expression vector comprising the isolated nucleic acid cited above, a host cell comprising the above cerecombinant nucleic acid cited above, a host cell comprising the above comprising at least 10 contiguous nucleotides of any of the above comprising at least 10 contiguous nucleotides of any of the above mentioned nucleotide sequences, an isolated polypeptide (encoded within an open reading frame of a CA sequence salected from any of the 95 polynucleotide sequences as mentioned in the specification, or its complement), an isolated antibody, (or its antigen binding fragment) that binds to the above polypeptide, a hybridom that produces the above antibody and a pharmaceutical composition comprising the above antibody and a pharmaceutical composition comprising the above antibody and a pharmaceutical excipient, a kit for detecting cancer colls (comprising the antibody cited above, methods for diagnosing cancer colls (comprising the presence or absence of cancer cells in an individual, a method for delivering a therapeutic agent to cancer cells in an individual, an electronic library comprising the above polymetide (or their fragments), methods of secreening correct associated with expression of a polymetide in a test cell sample, a method for treating cancers and a method for inhibiting the expression of a polymetide in a test cell sample, a method for treating cancers and a method for inhibiting cancers and a method sare useful for detecting, dagnosing, preventing and treating cancers, especially lymphoma and cancer the present sequence is a mouse CAP genomic sequence at the modulate cancer the present sequence is a mouse CAP genomic sequence associated with spearent did not form part of the printed cancer. The present sequence is a mouse CAP genomic sequence
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for diagnosing, preventing or treating cancers, especially lymphoma and leukemia, or in screening for agents that modulate cancer.
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                                                                         disclosure; seqid 545; 310pp; English.
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             26-JAN-1999;
17-JUL-2003.
                                                                    10-FEB-1998;
12-FEB-1998;
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10-FEB-1998
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19-FEB-1998
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neurological disease; Alzheimer's disease; Parkinson's disease; dementia;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             constructs for plant gene expression and transgenic plants. The nucleic acid molecules are also useful as markers or probes. The present sequence is a soybean EST (expressed sequence tag) from a gene encoding a sucrose pathway enzyme. Note: The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rinted specification, but was obtained in electronic format from USPTO at seqdata.uspto.gov/sequence.html?DocID=20030135870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ss; gene; osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic; gene therapy; diagnostic marker; morbid state; osteoporosis;
                                                                                                                                                                                                                                                                               New maize or soybean enzymes and nucleic acid molecules associated with the sucrose pathway, useful for genome mapping, gene identification and analysis, plant breeding, or preparation of constructs for plant gene
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                98US-00210297.
98US-0111981P.
98US-0113224P.
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                                                                                                               (CHEI/) CHEIKH N
(FISH/) FISHER D
(LIUJ/) LIU J.
                                                                            12-JAN-1999;
                                   11-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
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Pred. No. 2e+02;
0; Mismatches 3; Indels 0;
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09-MAY-2003; 2003JP-00131392.
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Isono Y,
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                                                     Homo sapiens.
                                                                                                          EP1440981-A2
                                                                                                                                                                  28-JUL-2004.
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cancer.
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NAME/KEY: sig_peptide
LOCATION: 290..361
IDENTIFICATION METHOD: Von Heijne matrix
OTHER INFORMATION: score 3.5
OTHER INFORMATION: seq_ALSLFYTADTSHG/SE
US-08-905-223-168
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FEATURE:
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Sequence 689, App
Sequence 649, App
Sequence 356, App
Sequence 6, Appli
Sequence 16539, A
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14757, A
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36, Appl
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1, Appli
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Sequence 15104, A
Sequence 109231,
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Sequence 14345,
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-976-594-356
US-09-949-016-16539
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US-09-949-016-115104
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US-09-949-016-11630
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Listing first 45 summaries
                                                           - nucleic search, using sw model
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Sequence 14033, A Sequence 213, App Sequence 136775, A Sequence 1369, A Sequence 1, Appli Sequence 1, Appli Sequence 11, Appli Sequence 11, Appli Sequence 16, Appli Sequence 15, Appli Sequence 15566, Sequence 155567, Sequence 155567, Sequence 155567, Sequence 155567, Sequence 155567,		
US-09-949-016-14033 US-09-495-016-76775 US-09-949-016-13453 US-09-949-016-13453 US-09-949-016-13969 US-08-319-8368-1 US-08-319-8368-1 US-08-319-8368-1 US-08-319-8368-1 US-08-319-8368-1 US-08-319-8368-1 US-08-319-8368-1 US-09-949-016-155566 US-09-949-016-155568 US-09-949-016-155568	ALIGNWENTS n US/08905223 Jean-Baptiste D. Aymeric Bruno 5, ESTS FOR SECRETED PROTEINS 503 S. Martens, Olson & Bear roadway N: Y Disk ompatible Win95 ATA: US/08/905,223	; ,655 ION; 50 168:
68.0 784019 4 67.2 8 4019 67.2 1119801 4 66.7 2 211049 4 66.4 4 66.4 4 66.1 4 66.4 6011 4	B. C.D. A. B. B. C.D. C. B. B. C.D. C. B. B. C.D. C. B. B. C. B. C	536 ORMATION , Ned A. BER: ORNBER: INFORMATI) 235-0176 235-0176 ID NO: ISTICS: CID NO: COUBLE OUBLE R R NA
C C 28	RESULT 1 US-08-905-223-168/c Sequence 168, Applicat Patent No. 622209 GENERAL INFORMATION: APPLICANT: Duclert APPLICANT: Duclert APPLICANT: Lacroix TITLE OF INVENTION: NUMBER OF SEQUENCES CORRESPONDENCE ADDR ADDRESSEE: ADDR ADDRESSEE: ADDR CONTENT: Californi COUNTRY: Californi COUNTRY: Californi CONPUTER: READABLE FI MEDIUM TYPE: FI COMPUTER: READABLE FO COMP	CLASSIFICATION: ATTORNEY/AGENT INF NAME: Israelsen REGISTRATION NUM REFERENCE/DOCKET TELECOMMUNICATION TELEFPAX: (619) INFORMATION FOR SEQ SEQUENCE CHARACTER SEQUENCE CHARACTER LENGTH: 436 bas TYPE: NUCLEIC A STRANDEDNESS: D TOPOLOGY: LINEA MOLECULE TYPE: CO ORIGINAL SOURCE: ORGANISM: HONO TISSUE TYPE: HONO
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US-09-976-594-356/c
US-09-976-594-356/c

Sequence 356, Application US/09976594

Fatent No. 6673549

GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
CURRENT APPLICATION NUMBER: US/09/976,594

CURRENT APPLICATION NUMBER: 60/240,409

PRIOR APPLICATION NUMBER: 60/240,409

PRIOR APPLICATION NUMBER: 60/240,409

NUMBER OF SEQ ID NOS: 1143

SOFTWARE: PERL PROGram
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 198008.8
US-09-976-594-356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74.4%; Score 18.6; I
84.0%; Pred. No. 35;
:ive 0; Mismatches
                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Incyte Pharmaceuticals, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3384 TCAGAACCATGGATGTATCAGCAG 3360
                                                                                                                                                                                                                                                                                                                                                                                   213 TCAGAACCATGGGATGTATCAGCAG 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 TCAGAACCCTGTGATGAATCAACAG 25
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CURRENT FILING DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pt_FL_genes Version 2.0
SEQ ID NO 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Vac, Henry
APPLICANT: COTLCY, Neil C.
APPLICANT: Guegler, Karl J.
APPLICANT: Baughn, Mariah
TITLE OF INVENTION: PROTEIN PI
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 3174 Forter Drive
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 84.0
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                         Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
                                                                                                               TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                   FEATURE:

NAME/KEY: CDS

LOCATION: (137)...(295)

US-09-799-451-649
                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
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STATE: Cali
COUNTRY: US
ZIP: 94304
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US-09-045-973-6
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                                                                                       LENGIH:
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                                                                                                                                                                                                                                  Sequence 689, Application US/09976594

GENERAL INFORMATION:

APPLICANT: Buchbinder, Jenny

TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS FILE REFERENCE: PA-0041 US

CURRENT APPLICATION NUMBER: US/09/976,594

CURRENT FILING DATE: 2000-10-12

PRIOR FILING DATE: 2000-10-12

NUMBER OF SEQ ID NOS: 1143

SOFTWARE: PERL PROGRAM

SEQ ID NO 689

LENGTH: 1067
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                    Score 18.6; DB 3; Length 436;
Pred. No. 20;
                                                                   4; Indels
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TITLE OF INVENTION: No. 6783969el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KET: misc feature

CTHER INFORMATION: Incyte ID No. 6673549 406289.1

NAME/KET: unsure

LOCATION: 17, 35, 40, 70, 496

OTHER INFORMATION: a, t, c, g, or other

US-09-976-594-689
                        Query Match
74.4%; Score 18.6; Di
Best Local Similarity 84.0%; Pred. No. 20;
Matches 21; Conservative 0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/799,451
                                                                                                                                          366 TCAGAACCATGGGATGTATCAGCAG 342
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Patent No. 6783969
GENERAL INFORMATION:
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: Ma, Yunqing
:: Yamazaki, Victoria
F: Chen, Rui-hong
"anq, Zhiwai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Tang, Y. Tom
APPLICANT: Zhou, Ping
APPLICANT: Goodzich, Ryle
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
APPLICANT: Zhang, Jie
APPLICANT: Xue, Aidong J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Yang, Yonghong
Wehrman, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zhao, Qing A.
Wang, Jian-Rui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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APPLICANT:
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Geguence 3362, Application US/09949016

patent No. 681239

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOD.307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FESTESEQ FOR Windows Version 4.0
                                                                                                                                                                                                                                                         APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THERENE ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THERENE ENCODING HUMAN KINASE PROTEINS, AND USES
FILE REFERENCE: CLOOLOG7
CURRENT APPLICATION NUMBER: US/09/751,389
CURRENT FILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PASLSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 786431
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Pred. No. 2.9e+02;
0; Mismatches 4; Indels 0;
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                                                           394 caraacccrerearrerreacae 417
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          2 CAGAACCCTGTGATGAATCAACAG
                                                                                                                                                                                 Sequence 3, Application US/09751389; Patent No. 6630334; GENERAL INFORMATION:
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; OTHER INFORMATION: n = A,T,C or
US-09-751-389-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.3%;
Matches 20; Conservative
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18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-949-016-3362
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Patent No. 6812339

GENERAL INFORMATION:
FAREAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FESTSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 3; Length 1729;
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/045,973
FILING DATE: Filed Herewith
CLASSIFICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                               PF-0491 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 CAGAACCCTGTGATGAATCAACAG 25
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16539
                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: B111ings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEPAX: (650) 845-4166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1729 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BRSTNOT16
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CLONE: 3041794
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LENGTH: 45684
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US-09-045-973-6
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Sequence 16430, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: 60/241,755
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR PELING DATE: 2000-10-20
FRIOR PELING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
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US-09-949-016-14757

US-09-949-016-14757

Sequence 14757, Application US/09949016

Sequence 14757, Application US/09949016

Sequence 14757, Application US/09949016

Sequence 14757, Application US/09949016

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PLING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-09-08

PRIOR PLING DATE: 2000-09-08
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Pred. No. 3.4e+02;
0; Mismatches 3;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              48942 GAAACCTGGGATGAATCAAAAG 48921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 CAGAACCCTGTGATGAATCAAC 23
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86.4%; Pred
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Best Local Similarity 86.45
Matches 19; Conservative
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Best Local Similarity
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ORGANISM: Human
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US-09-949-016-14757
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                  US-09-949-016-15104

Sequence 15104, Application US/09949016
Fatent No. 6812339
Fatent No. 6812339
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Fatent No. 6812330
Fatent No. 6812300
Fatent No. 681231
Fatent No. 6812300
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Patent No. 6812339
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| LOCATION: (1)...(33908)
| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15104
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Best Local Similarity 86.4
Matches 19; Conservative
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US-09-949-016-109231/c
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ORGANISM: Human
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APPLICANT: Tang, Y. Tor APPLICANT: Zhou, Ping

RESULT 11 US-09-949-016-16430/c

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Sequence 16928, Application US/09949016

Sequence 16928, Application US/09949016

Patent No. 6812339

GENERAL INPORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-3

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTHAME: FRASE FRASE FOR WINDOWS VERSION 4.0

SEQ ID NO 16928

LENGTH: 524032
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                                                                                                                                                                                                            Length 21706;
                                                                                                                                                                                             DB 3; Le...,
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80.0%; Pred. No. 5.2e+02;
                                                                                                                                                                                                        Query Match 68.0%; Score 17; DB Best Local Similarity 80.0%; Pred. No. 2.8e Matches 20; Conservative 0; Mismatches
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| LOCATION: (1)...(524032)
| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16928
TELEPHONE: (301) 309-8504
TELEPAK: (301) 309-8512
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 21706 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Best Local Similarity 80.0
Matches 20; Conservative
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ORGANISM: Human
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TOPOLOGY:
US-08-961-527-36
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                                                                                                                                                                                                                                                                                                                 APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 67383691 Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT APPLICATION NUMBER: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: PI FL_Genes Version 2.0
LENGTH: 6653
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Pred. No. 2.2e+02;
0; Mismatches 5
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Patent No. 6430135
GENERAL INFORMATION:
TITLE OF INVENTION: Streptococcus pneumonis
NUMBER OF SEQUENCES: 391
CORRESPONDENCE ADDRESS:
ADDRESSE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STAME: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1938 rcadaacagrcrgrrgaarcagcag 1962
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APPLICATION NUMBER: US/08/961,527
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REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PB340P1
TELECOMMUNICATION INFORMATION:
                                                                                                                                            Ma, Yunqing
Yamazaki, Victoria
Chen, Rui-hong
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80.0%;
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                                                                                 Xue, Aidong J.
Zhao, Qing A.
Wang, Jian-Rui
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Best Local Similarity 80.04
Matches 20; Conservative
  Goodrich, Ryle
Asundi, Vinod
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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MEDIUM TYPE: Diskett
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Feiyan
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; LOCATION: (1).
US-09-799-451-489
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                                                                                     APPLICANT
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02:00:36 ; Search time 1185.16 Seconds (without alignments) 129.102 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_MEW_PUB.seq:*
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13: /cgn2_6/ptodata/1/pubpna/USO9_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
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19: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*
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11: /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*
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16: /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*
17: /cgn2_6/ptodata/1/pubpna/USO0_NEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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25
1 tcagaaccctgtgatgaatcaacag 25
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Listing first 45 summaries
                                                                                                                                                OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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				2472	1	11	6	2	. 9	4	7	15	_	œ
SUMMARIES				US-10-808-187-2472	808-187-	808-187-	US-10-699-936-9	JS-10-889-447-5	JS-10-889-447-6	JS-10-889-447-4	JS-10-889-447-7	US-10-839-729-15	827-757-	JS-10-889-447-8
SCOM			Ω	US-10-	US-10-	US-10-	US-10-	US-10-	US-10-	US-10-	US-10-	US-10-	US-10-	US-10-
			DB	19	19	19	19	19	19	19	19	18	18	19
		Query	Length	25	646	1213	5262	28920	28920	29291	29430	29727	29727	29727
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ALIGNMENTS

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GREAT INFORMATION:

GRAPLICANT: PEIRIS, JOSEPH S. M.

APPLICANT: PUEN, KWOK YUNG

APPLICANT: TUEN, KWOK YUNG

APPLICANT: TOWN, LIT MAN

APPLICANT: GUAN, YI

APPLICANT: GLAN, KWOK HUNG

APPLICANT: CHAN, KWOK HUNG

TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE

TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE

TITLE OF INVENTION: RESPIRATORY SYNDROME (SARS)

TITLE OF INVENTION: RESPIRATORY SYNDROME (SARS)

TITLE OF INVENTION NUMBER: 60/457,031

PRIOR FILING DATE: 2003-03-26

PRIOR PLICATION NUMBER: 60/457,730

PRIOR PLICATION NUMBER: 60/459,311

PRIOR PLICATION NUMBER: 60/467,357

PRIOR PLILING DATE: 2003-04-03

PRIOR PLILING DATE: 2003-04-03

PRIOR PLILING DATE: 2003-04-03

PRIOR PLILING DATE: 2003-04-14

PRIOR PLILING DATE: 2003-04-14

PRIOR PLILING DATE: 2003-05-05

PRIOR PLILING DATE: 2003-05-05

PRIOR PLILING DATE: 2003-04-14

PRIOR PLILING DATE: 2003-05-05

PRIOR PLILING DATE: 2003-05-16
                              ; Sequence 2472, Application US/10808187; Publication No. US20050009009A1; GENERAL INFORMATION:
US-10-808-187-2472
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FEATURE:
NAME/KEY: CDS
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US-10-699-936-9/c
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US-10-808-187-11
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                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
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APPLICANT: BOON, LIT MAN
APPLICANT: GUAN, YI
APPLICANT: CHAN, KWOK HUNG
APPLICANT: NICHOLLS, JOHN
TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
TITLE OF INVENTION: RESPIRATORY SYNDROME (SARS)
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                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: Primer US-10-808-187-2472
                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 25; DB 19; Length 25; Best Local Similarity 100.0%; Pred. No. 0.055; Matches 25; Conservative 0; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/10/808,187

CURRENT PILING DATE: 2004-03-24

PRIOR PILING DATE: 2003-03-24

PRIOR PILING DATE: 2003-03-26

PRIOR PILING DATE: 2003-03-26

PRIOR PILING DATE: 2003-04-02

PRIOR PILING DATE: 2003-04-02

PRIOR PILING DATE: 2003-04-02

PRIOR PILING DATE: 2003-04-02

PRIOR PILING DATE: 2003-04-03

PRIOR FILING DATE: 2003-04-08

PRIOR FILING DATE: 2003-04-08

PRIOR FILING DATE: 2003-04-08

PRIOR FILING DATE: 2003-04-08

PRIOR FILING DATE: 2003-04-14

PRIOR FILING DATE: 2003-04-14

PRIOR PILING DATE: 2003-04-14

PRIOR PILING DATE: 2003-04-14

PRIOR PILING DATE: 2003-04-14

PRIOR PILING DATE: 2003-04-13

PRIOR PILING DATE: 2003-04-13

PRIOR PILING DATE: 2003-04-13

PRIOR PILING DATE: 2003-04-23

PRIOR PILING DATE: 2003-04-23

PRIOR PILING DATE: 2003-04-23

PRIOR PILING DATE: 2003-05-16

NUMBER OF SEQ ID NOS: 2476

SOFTWARE: PALENTIN VEN. 3.2
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Publication No. US20050009009A1
GENERAL INFORMATION:
APPLICANT: FUENS, JOSEPH S. M.
APPLICANT: YUEN, KWOK YUNG
APPLICANT: POON, LIT MAN
                                                                                                                  TYPE: DNA ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS: 2476
SOFTWARE: Patentin ver. 3.2
SEQ ID NO 2472
LENGTH: 25
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Sequence 9, Application US/10699936;
Sequence 9, Application US/10699936;
Bublication No. US20050095582A1
GENERAL INFORMATION:
APPLICANT: Gillian-Rose, Laura
APPLICANT: Scholl, David R.
APPLICANT: Wentworth, David E.
APPLICANT: Wentworth, David E.
APPLICANT: Wentworth, David E.
APPLICANT: Wentworth, David E.
APPLICANT: Scholl, Compositions and Methods for Detecting Severe Acute Respiratory;
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory;
TITLE OF INVENTION: Syndrome Coronavirus
TITLE OF INVENTION: Syndrome Coronavirus
CURRENT APPLICATION NUMBER: US/10/699,936
CURRENT FILING DATE: 2003-11-03
NUMBER OF SEQ ID NOS: 87
SOFTWARE PATENTIN version 3.2
SEQ ID NO 9
LENGTH: 5262
                                                                                                                                                                                                                                                                                                                                          APPLICANT: CHAN, KWOK HUNG
APPLICANT: NICHOLLS, JOHN
TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
TITLE OF INVENTION: RESPIRATIORY SYNDROME (SARS)
TITLE OF INVENTION: RESPIRATIORY SYNDROME (SARS)
CURRENT APPLICATION NUMBER: US/10/808,187
CURRENT FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: 60/457,031
PRIOR PLING DATE: 2003-03-26
PRIOR APPLICATION NUMBER: 60/459,931
PRIOR APPLICATION NUMBER: 60/460,357
PRIOR APPLICATION NUMBER: 60/460,357
PRIOR APPLICATION NUMBER: 60/461,265
PRIOR APPLICATION NUMBER: 60/461,265
PRIOR FILING DATE: 2003-04-14
PRIOR FILING DATE: 2003-04-15
PRIOR APPLICATION NUMBER: 60/464,886
PRIOR FILING DATE: 2003-04-15
PRIOR APPLICATION NUMBER: 60/464,886
PRIOR FILING DATE: 2003-05-05
PRIOR SPLING DATE: 2003-05-05
PRIOR PLING DATE: 2003-05-05
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ORGANISM: Human severe acute respiratory system virus
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US-10-808-187-11/c
; Sequence 11, Application US/10808187
; Publication No. US2005009009A1
; GENERAL INFORMATION:
                                                                                                                                                          APPLICANT: PEIRIS, JOSEPH S. APPLICANT: YUEN, KWOK YUNG APPLICANT: POON, LIT MAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 100.
Matches 25; Conservative
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 29430;
                                                                                                                                                                                                                                                                                APPLICANT: Bennett, C. Frank
APPLICANT: Jain, Ravi
TITLE DO INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
FILE REFERENCE: RTS-0685US
CURRENT APPLICATION NUMBER: US/10/889,447
CURRENT FILING DATE: 2004-07-12
PRIOR PPLING DATE: 2003-07-12
NUMBER OF SEQ ID NOS: 241
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Jain, Ravi
TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
FILE REPERENCE: RTS-068158
CURRENT APPLICATION NUMBER: US/10/889,447
CURRENT PILING DATE: 2004-07-12
PRIOR PPLICATION NUMBER: 60/486,670
PRIOR PILING DATE: 2003-07-12
NUMBER OF SEQ ID NOS: 241
SOFTWARE: FASESEQ for Windows Version 4.0
                             Indels
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100.0%; Score 25; DB 19;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 25; Conservative 0; Mismatches 0;
      Best Local Similarity 100.0%; Pred. No. 0.3 Matches 25; Conservative 0; Mismatches
                                                                                                                 17512 TCAGAACCCTGTGATGAATCAACAG 17488
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ORGANISM: SARS coronavirus isolate BJ02
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ORGANISM: SARS coronavirus isolate GZ01
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                                                                                                                                                                                                                       ; Sequence 4, Application US/10889447; Publication No. US20050075307A1; GENERAL INFORMATION:
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LENGTH: 29430
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TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
FILLE REFERENCE: RTS-0685US
CURRENT APPLICATION NUMBER: US/10/889,447
CURRENT FILING DATE: 2004-07-12
PRIOR FILING DATE: 2003-07-12
PRIOR FILING DATE: 2003-07-12
NUMBER OF SEQ ID NOS: 241
SOFTWARE: FastSEQ for Windows Version 4:0
SEQ ID NO 6
LENGTH: 28920
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                                                                                        Score 25; DB 19; Length 5262;
Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Jain, Ravi
TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
FILE REFERENCE: RTS-0685US
CURRENT APPLICATION NUMBER: US/10/889,447
CURRENT FILING DATE: 2004-07-12
PRIOR FILING DATE: 2003-07-12
NUMBER OF SEQ ID NOS: 241
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO S
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100.0%; Score 25; DB
Best Local Similarity 100.0%; Pred. No. 0.2
Matches 25; Conservative 0; Mismatches
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TYPE: DNA ORGANISM: SARS coronavirus Shanghai QXC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: SARS coronavirus isolate BJ03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: SARS coronavirus isolate BJ04
                                                                                                                                                                          1 TCAGAACCCTGTGATGAATCAACAG 25
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COTHER INFORMATION: n is any nucleotide
US-10-889-447-5
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Publication No. US20050075307A1
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
                                                                                                                                                                                                                                                                                                                           Sequence 5, Application US/10889447
Publication No. US20050075307A1
GENERAL INFORMATION:
                                                                                      100.0%;
ilarity 100.0%;
Conservative 0,
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Best Local Similarity
Matches 25; Conserv
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US-10-889-447-5/c
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US-10-889-447-6/c
                                             US-10-699-936-9
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APPLICANT: Gillim-Ross, Laura
APPLICANT: Gillim-Ross, Laura
APPLICANT: Taylor, Jill
APPLICANT: Taylor, Jill
APPLICANT: Taylor, Jill
APPLICANT: Taylor, Jill
APPLICANT: Taylor, Joseph D.
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
TITLE OF INVENTION: Syndrome Coronavirus
FILE REPERENCE: DHI-07986
CURRENT APPLICATION NUMBER: US/10/699,936
CURRENT FILING DATE: 2003-11-03
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Sequence 17, Application US/10839729;
Publication No. US20050002953A1
GENERAL INFORMATION:
APPLICANT: Jens Herold:
TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES:
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: BIOBANK. 013A
CURRENT FAPLICATION NUMBER: 05/10/839,729
CURRENT FILING DATE: 2004-05-04
PRIOR APPLICATION NUMBER: 60/468703
PRIOR FILING DATE: 2004-05-06
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 0.2;
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CURRENT APPLICATION NUMBER: US/10/889,447
CURRENT FILING DATE: 2004-07-12
RICH APPLICATION NUMBER: 60/486,670
PRIOR FILING DATE: 2003-07-12
NUMBER OF SEQ 1D NOS: 241
SOFTWARE: FastSEQ for Windows Version 4.0
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US-10-699-936-1
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US-10-889-447-8
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100.0%;
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
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Best Local Similarity 100..
Loca 25; Conservative
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CRGANISM: SARS Coronavirus
US-10-839-729-17
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nes 25; Conservative
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Publication No. US20050004071A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Charged Polysaccharides Resistant To Lysosomal Degradation During
TITLE OF INVENTION: Kidney Filtration And Renal Passage And Their Use To Treat Or
TITLE OF INVENTION: Prevent Infection By Coronaviruses
FILE REFERENCE: 11213-007-999
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Publication No. US20050075307A1

GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank

APPLICANT: Bannett, Ravi

TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION

FILE REFERENCE: RTS-0685US
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                                                                                                                                                      APPLICANT: JOHN HOLDS
APPLICANT: JOHN HEROLG
TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
TITLE OF INVENTION: AND METHODS OF USE
FILE REPERENCE: BIOBANK.013A
CURRENT APPLICATION NUMBER: US/10/839,729
CURRENT PILING DATE: 2004-05-04
PRIOR APPLICATION NUMBER: 60/468703
PRIOR FILING DATE: 2003-05-06
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US-10-827-757-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 25; DB
100.0%; Pred. No. 0.2
:ive 0; Mismatches
    17497 TCAGAACCCTGTGATGAATCAACAG 17473
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CURRENT FILING DATE: 2004-04-20
PRIOR PILING DATE: 2004-04-20
PRIOR FILING DATE: 2003-04-21
NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.2
SEQ ID NO 1
LENGTH: 29727
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 29727
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                                                                                                                 ; Sequence 15, Application US/10839729
; Publication No. US20050002953A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TYPE: DNA; ORGANISM: SARS Coronavirus
US-10-839-729-15
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Best Local S:
Matches 25
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Job time : 1187.16 secs
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APPLICANT: Scholl, David R.
APPLICANT: Wencworth, David E.
APPLICANT: Wencworth, David E.
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
TITLE OF INVENTION: Syndrome Coronavirus
FILE REFERENCE: DHI-07986
CURRENT APPLICATION NUMBER: US/10/699,936
CURRENT FILING DATE: 2003-11-03
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.2
SEQ ID NO 3
LENGTH: 29736
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Publication No. US20050075307A1
GENERAL INFORMATION:
APPLICANT: Jain, Ravi
TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
FILE REFERENCE: RTS-0685U5
CURRENT APPLICATION NUMBER: US/10/889,447
CURRENT FILING DATE: 2004-07-12
PRIOR FILING DATE: 2003-07-12
NUMBER OF SEQ ID NOS: 241
SOFTWARE: FastSEQ for Windows Version 4.0
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                Query Match 100.0%; Score 25; DB 18; Length 29736; Best Local Similarity 100.0%; Pred. No. 0.2; Matches 25; Conservative 0; Mismatches 0; Indels 0;
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CRGANISM: SARS CORONAVIRUS CUHK-W1
US-10-889-447-9
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; ORGANISM: SARS coronavirus CUHK-W1
US-10-699-936-3
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LENGTH: 29736
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ISB1-5F20 CH213-167 PM3-CT080

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AV660314 AV660341 AV660099 AV660041

AV660250 RPCI-24-2 abg50d07.

CL648225 CCL648225 CCL648225 CC475485 AV660316 AV660314 AV66031 AV66041 AV66041 AV66041 AV66041 AV6184 AW761184 AW761184 AW761184 AW761184 AW761184 AW761184 AW761184 AW761889 BE030053 BE030053 BW307189 BW307189 BW307189

CLCA685571 CL648225 CL648225 CR475485 AV660306 AV660316 AV660099 AV660041 AV66041 AV66041 AV66041 AV602509 BH126055 CL254009 BF324198 AW761184 AW761184 AW761184 AW761184 AW761389 BH307189 BH307189 BH307189 BH307189

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ALIGNMENTS

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CF412109 CH3#077_F
CA924034 MTU707_F
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CA924034 MTU706.F]
BUB35678 TO77B08 P
BZ033043 1Kf18f01.
CV23440 WSD1916.B
AL198061 Tetraodon
AG01259 Homo sapi
AW14475 ME000423.
AW44775 ME000423.
AW49774 Jc67h11.D
BX926690 BX926690
CL99621 ZMMSHF001
BU938208 AGMCCURT
CC227732 CH261-156
AZ601060 1M0419107
AZ601060 1M0419107
BM36263 UT-R-CN1-
                                                              May 16, 2005, 00:01:20 ; Search time 2823.44 Seconds (without alignments) 337.038 Million cell updates/sec
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        GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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1 tcagaaccctgtgatgaatcaacag
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SULT 1	
231380/c	1
NOTHINI	CF23138U DtaCn020G4G0414 Donlar cDN2 library from cambial zone Donilus alba
	5', mRNA sequence.
ESSION	CF231380
SION	CF231380.1 GI:33450809
WORDS	EST.
JRCE	Populus alba x Populus tremula
RGANISM	Populus alba x Populus tremula
.,	
<i>:</i>	
	rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
ERENCE	
AUTHORS	Dejardin,A., הפסופ-ט
PTTI.E	Filace,e. Expressed semience tags from poplar wood tissues - A comparative
	analysis from multiple libraries
JOURNAL	Plant Biol. 6 (1), 55-64 (2004)
MENT	Contact: Leple JC
	Unit of Forest improvement, Genetics and Physiology
	National Institute for Agricultural Research (INRA)
	Domaine de Limere, BP20619 ARDON, 45166 OLIVET CEDEX, FRANCE
	Tel: 33 02 38 41 78 00
	Fax: 33 02 38 41 78 79
	Email: Jean-Charles.Leple@orleans.inra.fr
	PCR PRimers
	FORWARD: TriplexA 5' CTCGGGAAGCGCGCCATTGTG 3'
	BACKWARD: TriplexB1 5' ATACGACTCACTATAGGGCGA 3'
	Plate: PtaC0020 row: G column: 4
	Seg primer: TriplexA 5' CTCGGGAAGCGCGCCATTGTG 3'.
ATURES	Location/Qualifiers
source	1633
	/organism="Populus alba x Populus tremula"
	/
	/BLIAIII="CIOIIE INRA /I/-I-B4" /dh wrof-"taxon.80863"
	/ sex="female"
	"cambial zone harvested
	/dev stage="3-years-old poplar trees grown in the nursery"
	/clone_lib="Poplar cDNA library from cambial zone"
	/note="A composite cDNA library was made with mRNA
	isolated from opposite and tension wood tissues
	corresponding to the cambial zone collected on the bark
	side after debarking the stem. In this respect, in
	addition to cambium cDNA, this library also contains very

young phloem and very young xylem cDNA. The sampling was

Mus muscu

AG462202 1

AZ601400 BM386263 AG462202 CNS043P7

CC227732 AW903308

4Z601060

AQ155366 BZ372477

BX926690

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CA924034 1inear EST 27-DEC-2002
MTU7CL.P1.A01 Aspen leaf cDNA Library Populus tremuloides CDNA,
                                                                                                                                                              CF412108
CH3#077_F12MF Canine heart normalized CDNA Library in pBluescript Canis familiaris cDNA clone CH3#077_F12 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Division of Genetic Medicine
Vanderbilt University
529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA
741: 615 936 2661
Fax: 615 936 2661
Finant Length: 1483 Std Brror: 0.00
Seq primer: MF: GTTTCCCAGTCACGACGTTG
High quality sequence start: 82
High quality sequence stop: 764.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Populus tremuloides (quaking aspen)
Populus tremuloides
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Malpighiales, Salicaceae, Saliceae, Populus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /notes="Organ: heart, Vector: pBluescript; Site_1: 5' of vector Not1; Site_2: 3' of vector EcoR1; Tissue source: dog heart (adult, 30 day - 40 day fetal), right and left atria and ventricle. Dog breed - mixed (beagle, German shepherd, pointer, Irish setter). Library construction:
                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis. I bases 1 to 90 at Yi, Y., Desai, R., Olarte, M., Henthorn, P. and George A.L. Expressed sequence tags from Canine heart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Canine heart normalized cDNA Library in
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   813 AGAACCCTGTGATGAATCACCA 834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2003)
Other_ESTs: CH3#077_F12MR
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                                                                                                                                                                                                                                                                                                                                                                         Canis familiaris (dog)
Canis familiaris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: George AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21; Conservative
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CF412108/c
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ORGANISM
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                                                                                                                                                                                                        DEFINITION
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TITLE
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COMMENT
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KEYWORDS
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CA924034
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/db_xref="taxon:9615"
/clone="CH3#077 F12"
/cell_type="heart"
/cell_type="heart"
/dev_alage="mixed developmental stages (adult, 30 day - 40 day fetal)"
done on 3 different tilted trees grown in the nursery.

CDNA were cloned in an oriented way into Sfil (A and B)
restriction sites. A one-step conversion of Lambda
TriplEx2 to the corresponding priplEx2 plasmid was done
via site-specific recombination at loxP sites (Clontech;
PCR Amplified using flanking primers and then sequenced on
a ABI3100 Genetic Analyser (Applied Biosystem)"
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Contact: George AL

Division of Genetic Medicine

Fax elso 316 2660

Fax: 615 316 2661

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria, Carnivora; Fissipedia; Canidae; Canis. (bases 1 to 843)
Yi,Y., Desai,R., Olarte,M., Henthorn,P. and George A.L. Expressed sequence tags from Canine heart (2003)
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                                                                                                                                                                                                                                                                                                                                      83.2%; Score 20.8; DB 7; Length 633;
88.0%; Pred. No. 83;
iive 0; Mismatches 3; Indels
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Canis familiaris
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DEFINITION

RESULT 2 CF412109 LOCUS

ACCESSION

VERSION KEYWORDS SOURCE

ORGANISM

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

Best Loc Matches

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ORIGIN

source

ORIGIN

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FEATURES

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Gaps

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Ralph.S., Cooper, D., Kolosova, N., Oddy, C., Butterfield, Y., Yang, G., Krikpatrick, R., Liu, J., Palmquist, D., Stott, J., Barber, S., Yang, G., Babakaiff, R., Brown-John, M., Chand, S., Featherstone, R., Masson, A., Mayo, M., Moran, J., Olson, T., Wong, D., Ritland, C.E., Siddiqui, A., Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C., Ritland, K. and Bohlmann, J.
                                                                BZ073043 700 bp DNA linear GSS 10-OCT-2002 lkf18f01.b1 B.oleracea002 Brassica oleracea genomic, genomic survey
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trichocarpa
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db xref="taxon:3712"
/clone_lib="B.oleracea002"
/note="Vector: pofwul3; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear pres uses oleracea TOHOODH3 buds provided by Thosmas Obborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Populus balsamifera subsp. trichocarpa (Populus trichocarpa)
Populus balsamifera subsp. trichocarpa
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Malpighiales, Salicaceae, Saliceae, Populus.
                                                                                                                                                                                                                Brassica oleracea
Sukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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                                                                                                                                                                                                                                                                                                 1 (bases 1 to 700)
Delehaunty, K., Fewell, G., Fulton, L., McCombie, W.R., Miner, T., Nash, W., Rabinowicz, P.D. and Wilson, R.K.
Whole genome shotgun reads from Brassica oleracea
Unpublished (2002)
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Pred. No. 1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                Genome Sequencing Center
Washington University School of Medicine
Bail: submissions@watson.wustl.edu
Plate: lkfi8 row: f column: 01
Seq primer: -21UPpOT forward
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High quality sequence stop: 551.
Location/Qualifiers
1..700
/organism="Brassica oleracea"
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                                                                                                                                               BZ073043.1 GI:23691559
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88.0%;
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Populus tremula x Populus tremuloides
Bukaryota, Viridiplantea; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
(Dases I to 675)
Unneberg, P., Bhalpianero, R.R., Jansson, S. and Sterky, F.
The poplar tree transcriptome: Analysis of expressed sequence tags
from multiple libraries
                                                                                                Confect: Tsai C-J.
Confect: Tsai C-J.
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources &
Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2915
Fax: 906 487 2915
Email: chtsai@mtu.edu.
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                 Ranjan,P., Kao,Y.-Y., Harding,S.A., Jiang,H., Joshi,C.P. and
Isai,C-J.
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/db_xref="taxon:47664"
/tissue_type="apical shoot"
/clone_lib="Populus apical shoot cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 270;
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/db_xref="texxon:3693"
/clone lib="Aspen leaf cDNA Library"
/note="Organ: leaf"
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Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupali.bhalerao@plantphys.umu.se.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 20.2; DB 6;
Pred. No. 1.4e+02;
0; Mismatches 3;
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Pred. No. 1.6e+02;

    .270
    /organism="Populus tremuloides"

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88.0%;
  (bases 1 to 270)
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Best Local Similarity 88.03
Matches 22; Conservative
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                                                                                       (2003)
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Genoscope.

Direct Submission

Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
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Homo sapiens genomic DNA, 21q region, clone: B269P7SpN28, genomic
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 649)

Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.

Homo sapiens genomic DNA, chromosome 21q

Published Only in DataBase (1998)

2 (bases 1 to 649)

Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.

Direct Submission
                                                                                                       Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetracdon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="G"
/note="Genoscope sequence ID : COAG140BA02SP1~end
PUC-Ori"
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Pred. No. 2.6e+02;
0; Mismatches 2;
Nat. Genet. 25 (2), 235-238 (2000)
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/db_xref="taxon:99883"
/clone="140A04"
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/db_xref="taxon:9606"
/chromosome="21"
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/clone="B269P7SpN28"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Jab_host="E. coli DH10B T1 phage resistant cells"
/ Jab_host="Pr-DX-N-A-10"
/ Jab_host="E. coli DH10B T1 SK (+) XR; Site 1: ECORI (5'
end of CDNA); Site_2: Xhol (3' end of CDNA); Outer xylem
from 5 year old trees harvested every two weeks between
April and october of 2002 at the University of British
Columbia south campus farm in Vancouver, British Columbia.

MRNA was isolated from each tissue source independently
and equal quantities of mRNA from each tissue were then
pooled. CDNA was prepared from 5 micrograms of mRNA and
directionally ligated into the pBluescript II SK (+) XR
vector using the pBluescript II XR CDNA Library
Construction Kit according to manufacturer's instructions
with modifications (Stratagene). Plasmid DNA was then
transformed by electroporation into DH10B cells
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Invitrogen) for propagation. Normalization was applied according to published methods (Bonaldo M.F. et al. (1996) Genome Research 6(9):791j in order to reduce the abundance of highly expressed transcripts."
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AL198061.1 GI:7836212
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Tetraccon nigroviridis
Bikaryota: Metaccoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetracontoidea; Tetracodontiformes;
                                                   Contact: Joers Bohlmann
Genome BC forest genomics program
Genome BC forest genomics program
Genome BC forest genomics program
UBC Biotechnology Laboratory, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 1Z3
Tel: 1-604-822-6028
Fax: 1-604-822-6097
Email: bohlmanneånterchange.ubc.ca
Plate: WS01916 row: H column: 19
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                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Populus balsamifera subsp. trichocarpa"
/mol type="mRNA"
/cultivar="WT-125"
/cultivar="WT-125"
/dub species="trichocarpa"
/db xref="taxon:3694"
/clone="WS01916_H19"
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                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 719
POLYA=Yes.
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      multiple cDNA libraries
Unpublished (2004)
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DEFINITION

RESULT 8 CNS02HTG

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/note="Vector: Uni-Zap XR vector, Stratagene (pBluescript SN,; Site 1: EcoRI, Site 2: Xho!; mRNA was extracted from eggs and the library was Constructed and excised according to the manufacturer's instructions."
                   Eukaryotes, Metazoas, Platyhelminthes; Trematoda; Digenea; Stristosoma.
Strigetidia; Schistosomatoidea; Schistosomatidae; Schistosoma.
1 (bases 1 to Saistosomatoidea; Schistosoma.
1 (bases 1 to Saistosoma mansoni genes with expressed sequence tags (cataloguing Schistosoma mansoni genes with expressed sequence tags (unpublished (1998)
Contact: Oliveira, Guilherme
Lab. Parasitologia Cel. e Mol.
Centro de Pesquisas Rene Rachou. FIOCRUZ
Av. Augusto de Lima 1715 Barro Preto, Belo Horizonte, MG, CBP 3010, Brazil.
Tel: 55 31 2953566
Fax: 55 31 2952115
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1 (bases 1 to 470)

Junqueira-de-Azevedo, I.L.M. and Ho, P.L.
A survey of gene expression and diversity in the venom glands of the pitviper snake Bothrops insularis through the generation of expressed sequence tagg (ESTs)

Gene 299 (1-2), 279-291 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /dev_stage="Egg"
/clone_lib="Egg stage cDNA expression library in Lambda
2APII"
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BM401974
EM401974.1 GI:20376603
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This EST corresponds to cluster BINI75A (see Reference)
Seg primer: M13F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 360;
                                                                                                                                                                                                                                                                                                                                   Email: oliveira@netra.cpgrr.fiocruz.br
Insert Length: 360 Std Error: 0.00
Seg primer: M13 Reverse Universal Sequencing primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Schistosoma mansoni"
/mol_type="mRNA"
/strain="LE"
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Instituto Butantan
Av. Vital Brazil, 1500, Sao Paul
Tel: 55 11 37 26 7222 ext. 2083
Fax: 55 11 37 26 1505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:6183"
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    Schistosoma mansoni
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MERONO'792.FER Egg stage cDNA expression library in Lambda ZAPII
Schistosoma mansoni cDNA 5' similar to EST AW146475 Egg stage cDNA
expression library, mRNA sequence.
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Schistosoma Metazoa, Platyhelminthes; Trematoda; Digenea;
Bukaryota; Metazoa, Platyhelminthes; Trematoda; Digenea;
Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.
I (bases 1 to 245)
Oliveira, G.C. and Baba, J.
Cataloguing Schistosoma mansoni genes with expressed sequence tags
Unpublished (1998)
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Lab. Parasitologia Cel. e Mol.
Centro de Pesquisas Rene Rachou - FIOCRUZ
Av. Augusto de Lima 1715 Barro Preto, Belo Horizonte, MG,
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                                            77.6%; Score 19.4; DB 9; Length 649; 95.2%; Pred. No. 3.8e+02; ive 0; Mismatches 1; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30190, Brazil
Tel: 55 31 2953566
Fax: 55 31 2952115
Email: oliveira@netra.cpgrr.fiocruz.br
Insert Length: 245 Std Brror: 0.00
Seq primer: M13 Reverse Universal Sequencing primer.
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/mol_type="mkNA"
/strain="LE"
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/sex="Mixed"
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                                                                                                                                                                                                                                                                                                                                                                                  mansoni, egg, mRNA sequence.
AW146475
AW146475.1 GI:6194382
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AW497769.1 GI:7119504
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Schistosoma mansoni
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                                          Query Match
Best Local Similarity 95.2
Matches 20; Conservative
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EST 01-MAY-2002

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BZ372477.1 GI:25457086
ch 76.8%;
1 Similarity 87.5%;
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Best Local Similarity
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                                                   /tissue_type="venom glands" /clone lib="seave bothrops insularis library IL3" /clone lib="snake Bothrops insularis library IL3" /note="Organ: venom glands; Vector: pGEMILZf+; Site_1: Bco RI; Site_2: Not I; Sug of mRNA from Bothrops insularis venom glands were primed with oligo-(dT) and reverse transcribed to cDNA using Superscript Plasmid System for cDNA Synthesis and Cloning (LifeTechnologies). The cDNAs were selected by size (350-600 pb and up 600 pb) in agarose gel electrophoresis, linked to Eco RI adapters and directionally cloned in pGEMILZf+ vector (Promega). ESTs were generated from random clones and grouped in unique sequences. The putative identification of each EST or cluster was obtained through Blast searches (e-value < e-05)."
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 474)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
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Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
                                                                                                                                                                                                                                                                                                                                                                                                  Score 19.2; DB 4; Length 470; Pred. No. 4.5e+02;
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
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/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Mahairas GG, Wallace JC, Hood L
        organism="Bothrops insularis"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 474.
Location/Qualifiers
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                           1 TCAGAACCCTGTGATGAATCAACA 24
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Plate: 3058 row: E colun
Class: BAC ends
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GSS.
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Best Local Similarity 87.5%;
Matches 21; Conservative
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Homo sapiens
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Enbryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade, Panicodeae; Andropogoneae; Zea.

1 (Dases 1 to 477)

1 (Dases 1 to 477)

1 (Bases 1 to 477)

2 Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N., Katzenburger, F., King, L., Miller, B., Muller, S., Nascimento, L., Zutavern, T., McCombie, W.R. and Martiensen, R.A. Genomic shotgun sequences from Zea mays (methyl-filtered)

1 Unpublished (2002)

2 Contact: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /lab host="DHSa" / Clone lib="WGS-ZmaysF (DH5a methyl filtered)" / Clone lib="WGS-ZmaysF (DH5a methyl filtered)" / Clone lib="WGS-ZmaysF (DH5a methyl filtered)" / Inote="Organ: immature ears, Site=1: Xba I; Site 2: Xba I; The vector was digested with XbaI and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (.x/y reads in Mi3mpl9, .b/g reads in pUCl9). The same ligation was transformed into DH5a."
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   Length 474;
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Score 19.2; DB 8;
Pred. No. 4.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                ie67h11 5', genomic survey sequence.
BZ372477
                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mccombie@cshl.org
Plate: ie67 row: h column: 11
Seq primer: -21Ml3UnivFwd
Class: shotgun
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                                                                                                                                                                         248 TCAGAACCCTGTGTTGATTAAACA 225
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Location/Qualifiers
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/dev stage="from embryos to adults"
/clone lib="Sus Scrofa library (scan)"
/clone="fissues: adipose tissue, brain, kidney, liver,
muscle, ovary, testis, heart, hypothalamus, pancreas,
skin, spleen, thymus, placenta, pituitary gland, seminal
sexicle, small intestine, uterus, adrenals, bulbo uretral
gland, cerebral trunk, epididymis, female gonad,
gall-bladder, hippocampus, large intestine, male gonad,
melanocytes, stomach, udder"
                                                                                                                                                                                                                                                                                                                                                                                                                                                cedex, FRANCE

ret: 33 (0) 5.61.28.51.14

Fax: 33 (0) 5.61.28.51.08

Email: tosser@toulouse.inra.fr

Clone distribution: AGENAE Resource centre. Francois PIUMI,

Francois.Piumi@jouy.inra.fr, INRA, CEA Radiobiologie et Etude du

genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex,

FRANCE, 433 (0) 1.34.65.28.02, 433 (0) 1.34.65.22.73

at sigenaende of vector, adaptator and repetitions. Contact us

sequence.
                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 532)
                                                                                                                                                                                                                                                                                                                                                               Genetique Animale
Institut National de la Recherche Agronomique
Chemin de Borde-Rouge - Auzeville BP27, 31326 Castanet-Tolosan
                                                                                                                                                                                                                           Bonnet, A., Tosser-Klopp, G., Benne, F., Cabau, C., Villeger, S., Soares, M., Bonaldo, F. and Hatey, F.
A Pig Normalised Multi-Tissue cDNA Library
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
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Location/Qualifiers
1. 532
/organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                        Contact: Tosser-Klopp G
        BX926690
BX926690.1 GI:41143538
                                                                                         Sus scrofa (pig)
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                            TITLE
JOURNAL
COMMENT
                                                                                                                                                                                           REFERENCE
AUTHORS
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Gaps 0 Query Match 76.8%; Score 19.2; DB 5; Length 532; Best Local Similarity 87.5%; Pred. No. 4.6e+02; Matches 21; Conservative 0; Mismatches 3; Indels (

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2 CAGAACCCTGTGATGAATCAACAG 25

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215 CAGAAACCTGAGATGAGTCAACAG 238

Search completed: May 16, 2005, 06:03:20 Job time : 2831.44 secs



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Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database

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-1. -. > 626
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GVITHDVSAJINRPGIGVVREFITRNPAMRKAVFISPYNSONAVASKILGLPFQTVDS
SQGSEYDFVIFTGTTETAHSCNVNRFNVAITFAKIGILCIMSDRDLYD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J., Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M. Arthur.

Vang, J.-Y., Chen, H.-Y. and Chen, Y.-M. Arthur.

Submitsed (28-0CT-2003) National Yang-Ming University, AIDS

Prevention and Research Center, 155, Li-Nong St., Sec.2, Peitou, Taipei, Taiwan 112, R.O.C.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                           SARS coronavirus TW-HP1
SARS coronavirus TW HP1
SARS coronavirus TW HP1
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.

1 (bases 1 to 626)
Lan,Y.-C., Chen,Y.-J., Lee,C.-M., Liu,T.-T., Lu,J.-J., Chan,Y.-J.,
Sang,J.-Y., Chen,H.-Y. and Chen,Y.-M. Arthur.
Molecular Epideniology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS
                  AY451928 626 bp RNA linear VRL 28-FEE
SARS coronavirus TW-HPl isolate TW-HPl_SC18 replicase 1B gene,
        AY534764
AY504470
AY304490
AY3046490
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AY309600
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                                                         May 15, 2005, 21:16:45; Search time 382.5 Seconds (without alignments) 2026.885 Million cell updates/sec
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        5.1.6
Compugen Ltd.
                                                                                                                                                               4708233 segs, 24227607955 residues
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        GenCore version (c) 1993 - 2005
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Maximum Match 100%
Listing first 45 summaries
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seq length: 200000000
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Match Length DB
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AY451931.1 GI:42741334
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GVITHDVSSAINREPQIGVVREFLTRNPAMRKAVFISFYNSQNAVASKILGLFTQTVDS
SQGSEDYVIFTQTTETAHSCNVNRFNVAITRAKIGILCIMSDRDLYD"
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1 (bases 1 to 626)
Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J., Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M. Arthur.
Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS
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SARS coronavirus TW-HP3
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
1 (bases 1 to 626)
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Direct Submission
Submitted (28-OCT-2003) National Yang-Ming University, AIDS
Prevention and Research Center, 155, Li-Nong St., Sec.2, Peitou, Inaiwan 112, R.O.C.
Location/Qualifiers
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   Length 626;
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Score 16; DB 14;
Pred. No. 1.3e+02;
; Mismatches 0;
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Query Match 100.0%; So
Best Local Similarity 100.0%; Pr
Matches 16; Conservative 0;
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SARS coronavirus TW-HP2
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AY451931 626 bp RNA linear VRL 28-FEB-2004 SARS coronavirus TW-HP4 isolate TW-HP4_SC18 replicase 1B gene, partial cds.
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GVITHDVSSAINRPQIGVVREFLTRNPAMRKAVFISPYNSQNAVASKILGLPTQTVDS
SQGSEYDYVIFTQTTETAHSCNVNRFNVAITRAKIGILCIMSDRDLYD"
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SARS coronavirus TW-HP4
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
1 (bases 1 to 626)
Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J.,
Rang, J.-Y., Chen, H.-Y. and Chen, Y.-M. Arthur.
Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS
Unpublished
2 (bases 1 to 626)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (28-OCT-2003) National Yang-Ming University, AIDS Prevention and Research Center, 155, Li-Nong St., Sec.2, Peitou, Taipei, Taiwan 112, R.O.C.
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                                                                                                                Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Cononavirus.

(Doses 1 to 626)
Lan,Y.-C., Chen,Y.-J., Lee,C.-M., Liu,T.-T., Lu,J.-J., Chan,Y.-J., Marghur.

Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS
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2. (bases 1 to 626)

Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J., Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M. Arthur.

Direct Submission

Submitted (28-OCT-2003) National Yang-Ming University, AIDS

Prevention and Research Center, 155, Li-Nong St., Sec.2, Peitou, Taipei, Taiwan 112, R.O.C.

Location/Qualifiers
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Yang,J.-Y., Chen,H.-Y. and Chen,Y.-M.Arthur.
Direct Submission
Submitted (28-OCT-2003) National Yang-Ming University, AIDS
Prevention and Research Center, 155, Li-Nong St., Sec.2, Peitou,
Taipei, Taiwan 112, R.O.C.
Location/Qualifiers
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cive 0; Mismatches 0;
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AY451934.1 GI:42741340
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SQGSEYDYVIFTQTTETAHSCNVNRFNVAITRAKIGILCIMSDRDLYD"
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SQGSEVDYVIFFQTPTFAHSCKNVNRFVNAITRAKIGILCIMSDRDLYD"
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SARS coronavirus TW-JC2
SARS coronavirus TW-JC2
Voluses; sRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
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Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS
Unpublished
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Direct Submission
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llarity 100.0%; Pred. No. 1.3e+02;
Conservative 0; Mismatches 0;
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SARS coronavirus TW-CD3
SARS coronavirus TW-GD3
Viruses, seRNA positive-strand viruses, no DNA stage; Nidovirales;
Viruses, seRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.

L (bases 1 to 626)
S Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J.,
Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS
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L Unpublished
L Descoin Tracing the Origin and Dissemination of SARS
E 2 (bases 1 to 626)
E 2 (bases 1 to 626)
E 2 (base, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J.,
Yang, J.-Y., Chen, Y.-Y. and Chen, Y.-M.Arthur.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EYFNSVCRLWKTIGEDMFLGTCRRCPAEIVDTVSALVYDNKLKAHKDKSAQCFRMFYK
GVITHDVSSAINRPQIGVVREFLTRNPAWRKAVFISPYNSQNAVASKILGLPTGTVDS
SQGSEYDYVIFTGTTETAHSCNVNRFNVAITRAKIGILCIMSDRDLYD"
                                          AX451936 626 bp RNA linear VRL 28-FEB-2004 SARS coronavirus TW-GD2 isolate TW-GD2_SC18 replicase 1B gene, partial cds.
                                                                                                                                                                                                                             Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.

1 (bases 1 to 626)

1 (bases 1 to 626)

Yang, J. -Y., Chen, Y. -J., Lee, C. -M., Liu, T. -T., Lu, J. -J., Chan, Y. -J., Yang, J. -Y., Chen, H. -Y. and Chen, Y. -M. Arthur.

Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS
Unpublished

2 (bases 1 to 626)
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Direct Submission

Submitted (28-OCT-2003) National Yang-Ming University, AIDS

Prevention and Research Center, 155, Li-Nong St., Sec.2, Peitou,
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100.0%; Pred. No. 1.3e+02;
iive 0; Mismatches 0;
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Location/Qualifiers
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SQGSEYDYVIFTGTAHSCNVNRFNVAITRAKIGILCIMSDRDLYD"
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SARS coronavirus TW-GD1
SARS coronavirus TW-GD1
Viruses; sRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus

1 (bases 1 to 626)
Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J.,
Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M. Arthur.
Molecular Epidemiology of SARS in Talwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished

2 (Dases 1 to 626)
Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J.,
Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M.Arthur.

Direct Submission
Submitted (28-0CT-2003) National Yang-Ming University, AIDS
Prevention and Research Center, 155, Li-Nong St., Sec.2, Peitou,
Taipei, Taiwan 112, R.O.C.
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100.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 0;
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100.0%; Pred. No. 1...
0; Mismatches
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/db_xref="taxon:264377"
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Matches 16; Conservative
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SQGSEYDYVIFTQTTETAHSCNVNRFNVAITRAKIGILCIMSDRDLYD"
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1 (bases 1 to 626)
Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J., Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M. Arthur.

Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS
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Direct Submission
Submitted (28-CTT-2003) National Yang-Ming University, AIDS
Prevention and Research Center, 155, Li-Nong St.; Sec.2, Peitou,
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1 (bases 1 to 626)
Lan,Y.-C., Chen,Y.-J., Lee,C.-M., Liu,T.-T., Lu,J.-J., Chan,Y.-J.,
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100.0%; Pred. No. 1.3e+02;
iive 0; Mismatches 0;
                 Pred. No. 1.3e+02;
                                       Mismatches
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Location/Qualifiers
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SQGSEYDYVIFTQTTETAHSCNVNRFNVAITRAKIGILCIMSDRDLYD"
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SQGSEYDYVIFTQTTETAHSCNVNRFNVAITRAKIGILCIMSDRDLYD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J., Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M. Arthur.
Molecular Epidemiology of SARS in Taiwan - Development of a Simple Methol for Tracing the Origin and Dissemination of SARS
Unpublished

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SARS coronavirus TW-GD4
Viruses; SSRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
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      Direct Submission
Submitted (28-OCT-2003) National Yang-Ming University, AIDS
Prevention and Research Center, 155, Li-Nong St., Sec.2, Peitou,
Taipei, Taiwan 112, R.O.C.
Location/Qualifiers
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100.0%; Pred. No. 1.3e+02;
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EYBSVCRLAKKTIGPDNETGCRRCRAPAIVDTVASALVYDNKARHKKARAKOKSAQCFKMFYK
GVITHDVSSAINREQUIGVVREPLTRNPAMRKAVFISFYNSQNAVASKILGLPTQTVDS
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Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M. Arthur.

Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS

Unpublished

2 (bases 1 to 626)

Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J., Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M. Arthur.

Direct Submission
Submitted (28-OCT-2003) National Yang-Ming University, AIDS Prevention and Research Center, 155, Li-Nong St., Sec.2, Peitou, Location/Qualifiers
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(Coronaviridae; Coronavirus.

(Loses I to 6.5)

Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J., Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M. Arthur.

Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS
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Liu,T.-T., Lu,J.-J., Chan,Y.-J.,
Liu,T.-T., Lu,J.-J., Chan,Y.-J.,
Yang,J.-Y., Chan,H.-Y. and Chen,Y.-M.Arthur.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             626 bp RNA linear VRL 28-FEE SARS coronavirus TW-YM2 isolate TW-YM2_SC18 replicase 1B gene, AY451941
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Pred. No. 1.3e+02;
Mismatches 0; Indels
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Best Local Similarity 100.0%; P.
Matches 16; Conservative 0;
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SARS coronavirus TW-YM2
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/codon start=1
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Lan, Y.-C., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J., Yang, J.-Y., Chen, Y.-J., Lee, C.-M., Liu, T.-T., Lu, J.-J., Chan, Y.-J., Yang, J.-Y., Chen, H.-Y. and Chen, Y.-M. Arthur.

Molecular Epidemiology of SARS in Taiwan - Development of a Simple Method for Tracing the Origin and Dissemination of SARS

L Unpublished

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S (bases 1 to 626)

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SQGSEYDYVLFYQTTETAHSCNVNRFNVAITRAKIGILCIMSDRDLYD"
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Coronaviridae; Coronavirus.
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100.0%; Pred. No. 1.3e+02;
ive 0; Mismatches 0;
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AY451942.1 GI:42741356
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	GenCore version 5.1.6)		83.8
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Adj39000 SARS coro	Abz51221 Aspergill	Aav31202 E. coli J	Abz13359 Arabidops	Abz83472 Toxicolog	Aac50256 Arabidops	Aac39069 Arabidops	Adq28938 Human CYP	Adq38182 Human L-P	Abz81308 Human dru	Acn42336 Human dia	Abn95647 Gene #214	Adp68991 Mouse ZAQ	Adg97931 Mouse can	Acn45212 Mouse gen	Acn44484 Mouse gen	Aas32996 DNA encod	Abn76875 Human ORF	Aac28376 Human sec	Aas32997 DNA encod
SUMMARIES	QI	ADJ39000	ABZ51221	AAV31202	ABZ13359	ABZ83472	AAC50256	AAC39069	ADQ28938	ADQ38182	ABZ81308	ACN42336	ABN95647	ADP68991	ADQ97931	ACN45212	ACN44484	AAS32996	ABN76875	AAC28376	AAS32997
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	Score	16	15	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14	14	13.4	13.4	13.4	13.4
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Adr651330 Bacterial Adr63428 Cotton cD Ad4655780 Novel can Ad791696 Novel S. Ad13574 Human PRP Ad861997 Bacterial Ad861997 Bacterial Ad861997 Bacterial Ad761681 A gossayp Abc14524 Escherich ABC14374 Nucleotid Abt14524 Escherich Ad891977 Propionib Adf602304 Bacterial Adf602304 Bacterial Adf602304 Bacterial Adf602304 Bacterial Ad5615 Neospora Adf6945 Photorhab AbS54243 A. Sojae Ad89543 Brocdes m Ad925201 C. pneumo Ad30911 Frokaryot Ad209914 Human S' Ad889066 Human SDC	VTS				modified ribonucleotide; hepatitis C virus; HCV; hepatitis C; c; virucide; hepatitis A virus; E virus; Ebola virus; influenza virus; us; poliovirus; human papilloma virus; us; viral infection; gene; ds.								ANA, useful for treating viral as virus or coronavirus infection.		all interfering RNA (siRNA) which where the siRNA is resistant to lbit viral replication. Also in a patient; (2) making a modified quence in a virus; (3) a double-
ADS51330 ADR63428 AAH901625780 ADR55780 ADR35774 ADS60827 ACA50827 ACA508287 ACA508287 ACA508287 ACA508287 ACA508287 ACA508287 ACA508287 ACA508287 ACA30811 ACA508287 ACA30811 ACA30811	ALIGNMENTS	51 BP.		sequence.	", modified ri ", hepatitis C lic, virucide; E virus; Ebo rus; poliovir rus; viral in								terfering RNA, C, influenza v	English.	bes a smale lectide, y to inh: a virus : acid sec
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		standard; DNA;		virus	interfering RNA replication inh flammatory; hep tis D virus; herus; reovirus; cumoniavirus; c	oronavirus.	47-A1.	4.	٠.	CHIRON CORP	MY,	143862/1	resistant 3, e.g., h	Fig 3,	inv mod etai (1) targ
44444444444444444444444444444444444444			7390 MA	SS S	viral replication viral replication antiinflammatory; hepatitis D virus; rotavirus; reovirus metapneumoniavirus	SARS coron	WO20040116	-FEB-200 -JUL-200	-JUL-2002	(CHIR) CH	пJ, Seo	1; 2004-1	RNase	Example 10	presen orises se and cribed:
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		RESI ADJ. ID	S X E	BXB	X & & & & & & & & & & & & & & & & & & &	8 X	Z X	OY XX	X E !	X & S	¥ II \$	1 83	\$ E E \$	SS X	\$ 88888

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             hepatitis C virus (HCV); (4) inducing targeted RNA interference toward HCV in hepatic cells; (5) inhibiting replication of HCV; (6) a vector comprising a DNA segment encoding the RNA molecule; (7) a host cell comprising the vector of (6); (8) inhibiting replication of HCV; (9) exarying HCV; (9) treating hepatitis C in a subject; (10) a modified sirNA molecule comprising a double-stranded RNA molecule of 10:30 nucleotides in length, which mediates RNA interference toward a target agent or virus and is linked to at least one receptor-binding ligand; and (11) inducing targeted RNA interference in a patient. The modified siRNA molecules are useful for inactivating virus in mammalian cells. The siRNAs are useful for treating hepatitis C virus, hepatitis A
                                                                                                                                                                                                                                     virus, hepatitis D virus, hepatitis E virus, Ebola virus, influenza virus, vicaxirus, necarius, necarius, human papilloma virus, rocaxirus, necarius, human papilloma virus, metapneumoniavirus or coronavirus infections. The methods of the invention can be used to correct or compensate for cellular physiological abnormalities involved in conferring susceptibility to viral infections in patients and/or alleviate symptoms of a viral infection in patients. The present sequence represents the SARS coronavirus nucleotide sequence,
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stranded RNA molecule of 10-30 nucleotides that inhibits replication of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Abe K;
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Kobayashi T, Kitamoto N, Gomi K,
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(NORQ ) NAT FOOD RES INST MIN AGRIC.
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The invention relates to a polynucleotide having any of 6006 specific sequences (ABZ50888-ABZ56893), which are expressed by a fungus under specific culture conditions including one or more of eutrophic,

Claim 1; SEQ ID NO 334; 48pp + Sequence Listing; Japanese

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a E. coli strain J96 contig containing pathogenicity island (PAI) sequences, and represents a nucleic acid molecule of the invention. PAIs are large fragments of DNA which comprise pathogenicity determinants. The sequences of the invention are taken from PAI IV and PAI V. PAI IV is located at approximately 64 min (near pheV) on the E. coli chromosome and is greater than 170 kb. PAI V is located at approximately 94 min (at pheR) on the E. coli chromosome and is approximately 160 kb in size. Antibodies specific to the proteins encoded by the PAI open reading frames of the invention can be used in kits to detect uropathogenic E. coli. The proteins are used in vaccines to elicit a protective immune response in an animal to the uropathogenic E. coli
oligotrophic, solid, early germination, alkaline, high temperature, low temperature or maltose culture or polymucleotides stringently hybridising to these sequences. The polymucleotides are useful for monitoring the progress of fermentation and the growth conditions of a fungus, especially of Aspergillus oryzae which is widely used in industrial fermentation. Also monitoring for fungal contamination. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          coli nucleotide sequences - used to develop pathogenic \boldsymbol{E}. coli and to elicit an immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PAI; pathogenicity island; uropathogenic E. coli detection; PAI IV; pheR; PAI V; pheV; vaccine; protective immune response; ds.
                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 746 BP; 203 A; 150 C; 188 G; 201 T; 0 U; 4 Other;
                                                                                                                                                                                                                    Length 875;
                                                                                                                                                                                   Sequence 875 BP; 223 A; 219 C; 227 G; 204 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                  DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E. coli J96 pathogenicity island contig #16.
                                                                                                                                                at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                    Score 15;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 21; Page 117; 250pp; English.
                                                                                                                                                                                                       93.8%; Scc...
100.0%; Pre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated uropathogenic E. c
products for the detection of p
response to pathogenic E. coli.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  97WO-US021347.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96US-0031626P
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                                                                                                                                                                                                                                                                                                                          661 rcreceraeccaarc 647
                                                                                                                                                                                                                                                                                                                                                                                                                  AAV31202 standard; DNA; 746
                                                                                                                                                                                                                                                                                         15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                         1 TCTGCGTAGGCAATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UYWI-) UNIV WISCONSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-312461/27.
                                                                                                                                                                                                                                  Local Similarity
les 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9822575-A2
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                                                                                                                                                                                                                  Query Match
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ABZ13359/

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The present invention describes a method (M1) for determining a toxicological response to an agent, which comprises comparing the expression profile of one or more human toxic response genes to a reference gene expression profile indicative of toxicity, and so determining the presence of a toxic response to the agent. Also ceremining the presence of a toxic response to the agent. Also comparibed: (1) an array comprising one or more polymolecides selected from the genes corresponding to the partial sequences given in ABZ82842 cto ABZ84764, or their fragments of at least 20 nucleotides, or homologues cresponse gene plays a role on toxic response pathways by determining the expression profile of the gene after exposure of cells or a human subject or a known toxic pharmaceutical or industrial agent, comprising (a) exposing cells to an agent or isolating cells from a human subject who exposing cells to an agent or isolating cells from a human subject who can appear or isolating the test gene expression profile to the expression profile to the expression profile of a gene with a similar function or comparing the test profile to the expression profile of a gene with a similar function or profile to the expression profile of a gene with a similar function or comparing the test profile to the expression profile of a gene with a similar function or predicting and determining toxicological responses on a cellular, organ or system level. The arrays comprising the human genes are useful for toxic toxicological screening of drugs, pharmaceutical compounds and chemicals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Determining a toxicological response to an agent, useful for screening of drugs, comprises comparing the expression profile of one or more human toxic response genes to a reference gene expression profile indicative of
                                                                                                                                                                                 Toxicologically relevant gene; toxicological response; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                   Toxicologically relevant human nucleotide sequence #631.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kier LD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neft RE, Dunn RT, Adkins K, Pickett GG,
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PHAS-) PHASE-1 MOLECULAR TOXICOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 215; 455pp; English.
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                                                                                                                                                                                                                                                                                                                                                                16-AUG-2002; 2002WO-US026514.
                                                                                                                                                                                                                                                                                                                                                                                                             16-AUG-2001; 2001US-0313080P.
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                                                                                      (first entry)
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                                                                                                                                                                                                                                                                       WO2003016500-A2.
                                                                                      14-MAY-2003
                                                                                                                                                                                                                                                                                                                    27-FEB-2003.
                                             ABZ83472;
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                                             요
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention. Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to identifying a stress condition to which a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cell has been exposed, comprising: (a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and (b) detecting a profile of expressed polynucleotides in the plant cell
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                           Length 746;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana stress regulated gene SEQ ID NO 1164.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana; plant; gene; stress; transgenic; ds
                                                                                      Indels
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                                      90.0%; Score 14.4; DB 2;
ilarity 93.8%; Pred. No. 2e+02;
Conservative 0; Mismatches 1;
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; Mismatches
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ABZ13359 standard; DNA; 801 BP
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                                                                                                                                                           334 TCTGCGTAGCCAATCC 319
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26-JAN-2001; 2001US-0264647P.
22-JUN-2001; 2001US-0300111P.
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                                                                                                                              1 TCTGCGTAGGCAATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana.
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                                                              Similarity
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les 15; Conserv
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Query Match
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21-JUN-1999
Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
           Arabidopsis thaliana DNA fragment SEQ ID NO: 64154
                                                                                                                                                                                  9905-0121825P.
9905-0123160P.
9905-0125788P.
9905-0126784P.
9905-0126784P.
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9905-0128744P.
9905-013884P.
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                                                                                                                                                             2000EP-00301439
                                                                                    Arabidopsis thaliana
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16-JUN-1999;
16-JUN-1999;
17-JUN-1999;
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18-JUN-1999;
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18-JUN-1999;
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21-APR-1999;
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23-APR-1999;
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99US-0121825P.
99US-0123180P.
99US-0125784BP.
99US-0126264P.
99US-0126785P.
99US-0126785P.
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99US-0129845P.
99US-0130077P.
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99US-0130891P.
99US-0131449P.
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99US-0132407P.
99US-0132484P.
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99US-0132863P.
99US-0134256P.
99US-0134218P.
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99US-0134221P.
99US-0134370P.
99US-0134768P.
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99US-0135339.
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99US-0136021P.
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99US-0139452P.
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99US-0140823P.
99US-0140991P.
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99US-0136782P
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99US-0140353P
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  Arabidopsis thaliana.
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14-MAY-1999;
14-MAY-1999;
18-MAY-1999;
19-MAY-1999;
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04-MAY-1999;
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10-JUN-1999;
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07-JUN-1999
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99US-0151080P.
99US-0151303P.
99US-0151313P.
99US-0153313P.
99US-015376P.
99US-015376P.
99US-015376P.
99US-015376P.
99US-015473P.
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99US-0155139P.
99US-015523P.
99US-015523P.
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99US-015923P.
99US-015923P.
99US-015923P.
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99US-015923P.
99US-015933P.
99US-015933P.
99US-016938P.
99US-016098P.
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Best Local Similarity
Matches 15; Conservat
27-AUG-1999;
30-AUG-1999;
11-AUG-1999;
07-SEP-1999;
10-SEP-1999;
11-SEP-1999;
15-SEP-1999;
16-SEP-1999;
20-SEP-1999;
22-SEP-1999;
23-SEP-1999;
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29-SEP-1999;
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R 30-40x-1999; 9918-0141287P.

R 01-JUL-1999; 9918-0141287P.

R 02-JUL-1999; 9918-0142184P.

R 02-JUL-1999; 9918-0142187P.

R 06-JUL-1999; 9918-0142803P.

R 11-JUL-1999; 9918-0142803P.

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R 11-JUL-1999; 9918-014237P.

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R 11-JUL-1999; 9918-0144333P.

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R 11-JUL-1999; 9918-0144333P.

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R 11-JUL-1999; 9918-014931P.

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R 11-JUL-1999; 9918-01493P.

R 11-JUL-1999; 9918-01493P.

R 11-JUL-1999; 9918
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Human; CYP1A2; Cytochrome P450; monooxygenase; enzyme; drug metabolism;
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Pred. No. 2.1e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADQ28938 standard; cDNA; 2169
9908-0154018P.
9908-0154039P.
9908-0155139P.
9908-0155139P.
9908-0155686P.
9908-0155686P.
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9908-015763P.
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9908-0159234P.
9908-0159634P.
9908-0159634P.
9908-016964P.
9908-0160744P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 93.8 es 15; Conservative
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15.58P-1999;
16.58BP-1999;
22.58BP-1999;
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29.0CT-1999;
20.0CT-1999;
20.0CT-1999;
20.0CT-1999;
21.0CT-1999;
22.0CT-1999;
22.0CT-1999;
23.0CT-1999;
24.0CT-1999;
25.0CT-1999;
26.0CT-1999;
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Matches
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hydratase/3-hydroxyacyl-CoA dehydrogenase bifunctional enzyme (L-PBE).

Also described: (1) an antibody specific for the canine L-PBE polypeptide; (2) an isolated polypucleotide comprising at least 12.

In NO:1 (S1, ADQ38172), or its fragment comprising at least 12.

Consecutive nucleotides of S1 or the non-coding strand complementary to it with the provision that the fragment comprises a mucleotide sequence that differs from any portion of the sequences of 2169, 2154, or 2166 bp (see SEQ ID No:11, 13 and 15, ADQ38182, ADQ38184 and ADQ38186), and from nucleotide sequence their complementary strands by at least one nucleotide; (3) an array of nucleic acid molecules, attached to a solid support, the array comprising concerned sequence that encodes a polypeptide comprising an amino acid sequence that is at least 95% homologous to P1 (see SEQ ID No:2, ADQ38173) and which encodes a polypeptide having L-PBE activity; (5) a method for determining the amount of canine L-PBE polynucleotide present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antiinflammatory; antianaemic; thrombolytic; antilipeemic; antidiarrheic; antiatteriosclerotic; antiasthmatic; immunosuppressive; antityroid; cytostatic; hepatotropic; virucide; dermatological; antidiabetic; nephrotropic; antigout; neuroprotective; thyromimetic; osteopathic; antiarthritic; antipsoriatic; uropathic; ophthalmological; antirheumatic; haemostatic; gene therapy; cell proliferative disorder; cancer; developmental disorder; endocrine disorder; edsorder; autoimmune disorder; gastrointeetinal disorder; liver disorder; autoimmune disorder; inflammatory disorder; liver disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           within a sample derived from a dog; (6) a method for measuring the metabolic response to a test agent in a dog; and (7) a method for determining the amount of canine L-PBE polypeptide present within a sample. The canine L-PBE polypeptide and polymoleotide are useful for measuring the metabolic response to a test agent in a dog. The present sequence encodes human L-PBE, which is used in an example from the present invention. The human L-PBE gene is located on chromosome 3, more
  New isolated canine peroxisomal enoyl-CoA-hydratase:3-hydroxyacyl-CoA dehydrogenase bifunctional enzyme (L-PBE), useful for measuring the metabolic response to a test agent in a dog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human drug metabolising enzyme, DME-8, coding sequence, SEQ ID 21.
                                                                                                                                                            The present invention describes the canine peroxisomal enoyl-CoA-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2169 BP; 589 A; 487 C; 546 G; 547 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; drug metabolising enzyme; anti-HIV; antiallergic;
                                                                                                           Claim 3; SEQ ID NO 11; 69pp; English
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/product= "DME-8"
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Matches
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                                                                                                                                                                                                    New isolated canine CYPIA2 polypeptide, useful for hybridization assays to detect the capacity of cells to express canine CYPIA2 or for measuring levels of canine CYPIA2 expression.
                                                                                                                                                                                                                                                                                                                                                      The present invention relates to canine CYPIA2 (Cytochrome P450, subfamily I, member A2) protein (ADQ28931) and coding sequence (ADQ28930). CYPIA2 is a microsomal cytochrome P450 dependent monooxygenase which functions in drug metabolism. The sequences useful in hybridization assays to detect the capacity of cells to express canine CYPIA2 or to measure levels of canine CYPIA2 expression. The present sequence was used in a sequence alignment with the canine CYPIA2 coding sequence. Note: This sequence alignment with the canine CYPIA2 coding sequence is the SEQ ID 9 shown in the sequence differs from the SEQ ID 9 shown in Fig 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          roxisomal enoyl-CoA-hydratase/3-hydroxyacyl-CoA dehydrogenase; L-PBE; functional enzyme; enzyme; metabolic response; human; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       90.0%; Score 14.4; DB 12; Length 2169; 93.8%; Pred. No. 2.2e+02; ive 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2169 BP; 589 A; 487 C; 546 G; 547 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding cDNA SEQ ID NO:11.
                                                                                                                                                                                                                                                                                                           Claim 3; SEQ ID NO 9; 64pp; English.
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/product= "L-PBE"
                                                   (PHAA ) PHARMACIA & UPJOHN CO.
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31-DEC-2002; 2002US-0437602P.
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les 15; Conservative
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GENBANK; NM_001966.
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ADQ38182;

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ADQ38182/c

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WO2004023973-A2
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                                                                                                                                                                                                                  Peralta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to novel human drug metabolising enzymes, DME-1 to DME-13 (ABP59210-ABP59222) and their coding sequences (ABZ81301-ABZ81313). The sequences are useful for diagnosing, treating or preventing disorders associated with aberrant expression of DME.

CC ARZ81313). The sequences are useful for diagnosing, treating or preventing disorders associated with aberrant expression of DME.

CC atherosclerosis, cirrhosis, paroxymeal nocturnal haemoglobinutia, polycythaemia vera, psoriasis, paroxymeal nocturnal haemoglobinutia, polycythaemia vera, psoriasis, paroxymeal nocturnal haemoglobinutia, cavelopmental disorders (e.g. renal tubular acidosis, anaemia or mental retardation), endocrine (e.g. osteoporosis, thrombosis, diabetes), eye disorders (e.g. osteoporosis, diabetes), eye disorders (e.g. osteoporosis, diabetes), eye disorders (e.g. osteoporosis, diabetes), or, cystic fibrosis), gastrointestinal disorders (e.g. dyperlipidaemia, cystic fibrosis), juver disorders (e.g. hyperlipidaemia, cautoimmune thyroiditis, contact dermatitis, Crohn's disease, autoimmune thyroiditis, contact dermatitis, Crohn's disease, cylomerulonephritis, Goodpasture's syndrome, multiple solerosis, osteoarthritis, pancreatitis, Reiter's syndrome, multiple solerosis, cortect of expension, uveitis). They are also useful in the assessing the effects of exogenous compounds on the expression of nucleic acid and amino acid sequences of DME. The polynucleotides encoding DME are useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene; gene therapy; human diagnostic and therapeutic polynucleotide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                         New drug metabolizing enzymes (DME) useful for diagnosing, treating preventing diseases or conditions associated with aberrant DME expression, e.g. cancer, AIDS, atherosclerosis, diabetes, glaucoma,
                                                                                                                                           Ramkumar J, Emerling BM, Richardson TW, Li JX;
Honchell CD, Baughn MR, Tang YT, Lee EA, Elliott VS
S, Swarnakar A, Porsythe IJ, Sanjanwala MM, Yao MG;
Y, Gorvad AE, Becha SD, Burford N;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human diagnostic and therapeutic polynucleotide SEQ ID NO:1211.
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                                                                                                                                                                                                                                                                                                                                   Claim 5; Page 177-178; 181pp; English.
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                                                                                                                                                       Warren BA, Honchell CD, Bau
Yue H, Lee S, Swarnakar A,
Zebarjadian Y, Gorvad AE, B
                                                      13-JUL-2001; 2001US-0305402P.
27-JUL-2001; 2001US-0308158P.
14-SEP-2001; 2001US-0322127P.
                                           06-JUL-2001; 2001US-0303745P.
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             05-JUL-2002; 2002WO-US021105
                                                                                                                (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                        hepatitis or osteoporosis.
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hes 15; Conservative
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P-PSDB; ABP59217.
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                                                                                                                                          Griffin JA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to novel diagnostic and therapeutic polynucleotides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New diagnostic and therapeutic polynucleotides and polypeptides, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in diagnosing a condition, disease or disorder associated with human molecules, e.g. autoimmune or inflammatory disorders, in gene therapy
                                                                                                                                                                                                                                                                                                                          Wright RJ, Bruns CM, Marjanovic MM, Shen F;
Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
Delegeane AM, Panear IS, Banville SC, Reddy TP;
Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
Anderson SB, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
Shiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
SM, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietze
Shi X, Suarez CJ;
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Pred. No. 2.4e+02;
0; Mismatches 1; Indels 0;
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                                                                      12-SEP-2003; 2003WO-US028227.
                                                                                                                                             12-SEP-2002; 2002US-0410259P.
12-SEP-2002; 2002US-0410260P.
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nes 15; Conservative
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                                                                                                                                                                                                                                                           (INCY-) INCYTE CORP.
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S, Shi X,
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Harthshorne TA,
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25-MAR-2004
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Horne D,

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The invention comprises a mammalian embryonic stem cell that has an inactivated ZAQ gene. The invention also comprises a non-human animal that is incapable of expressing the ZAQ gene. The embryonic stem cell of the invention is useful for screening a substance capable of preventing or treating gastrointestinal disorders, endocrinopathy, gonad disease, cancer, immunodeficiency disease, and neurological disease. The non-human animal of the invention is useful for screening a compound which promotes or inhibits the promoter activity of the ZAQ gene. The present DNA
                                                                                                                                                                                                                                                                                                                                                                                        Novel embryonic stem cell comprising inactivated ZAO gene, useful for screening therapeutic agent of gastrointestinal disorders, cancer and neurological disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence encodes the mouse ZAQ protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 7; SEQ ID NO 2; 52pp; Japanese.
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/number= 1
7539. .8232
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Best Local Similarity 93.8
Matches 15; Conservative
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P-PSDB; ADP68990.
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                                                                                                                                                                                                                                                                                                                          Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a liver tissue sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to a novel method for diagnosing and detecting the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mammalian embryonic stem cell; non-human animal model; inactivated ZAQ; ZAQ; gastrointestinal disorder; endocrinopathy; gonad disease; cancer; immunodeficiency disease; neurological disease; mouse; murine; gene; ds.
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93.8%; Pred. No. 2.40+0?
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/product= "Mouse ZAQ protein #1"
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0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 2145; 298pp; English.
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                                                                                                       02-OCT-2001; 2001WO-US030589.
                                                                                                                                                02-OCT-2000; 2000US-0237054P.
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Best Local Similarity 93.8<sup>†</sup>
Matches 15, Conservative
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                                                                                                                                                                                            (GENE-) GENE LOGIC INC.
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                    WO200229103-A2.
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Indels

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The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of bidding to Carcinoma Associated Protein (CAP); (iii) for screening of bioactive agent capable of modulating the activity of CAP; (iv) for a bioactive agent capable of modulating the activity of CAP; (iv) for carcinoma; (vi) for inhibiting the activity of CAP; (vi) for diagnosing carcinoma; (vii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing acrcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent
New isolated cancer associated nucleic acids comprising at least 10 contiguous nucleotides, useful for diagnosing, preventing and/or treating cancers such as leukemia and lymphoma.
                                                                                                                       The present invention relates to cancer associated sequences (ADQ97025-ADQ98004). The sequences are useful for the diagnosis, prevention and/or treatment of cancer, such as leukemia and lymphoma. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formate directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
                                                                                                                                                                                                                                                                        Sequence 68820 BP; 17966 A; 14439 C; 15095 G; 20194 T; 0 U; 1126 Other;
                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                             Query Match 90.0%; Score 14.4; DB 12; Length 68820; Best Local Similarity 93.8%; Pred. No. 3.2e+02; Matches 15; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatic; carcinoma; lymphoma; cancer; murine; gene; ss.
                                                                                  Claim 1; SEQ ID NO 908; 199pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 2047; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACN45212 standard; DNA; 68497 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                           20254 TTTGCGTAGGCAATCC 20269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mouse genomic sequence mCG9808
                                                                                                                                                                                                                                                                                                                                                                                                    16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2002; 2002US-00087192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                1 TCTGCGTAGGCAATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-328604/31.
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Sequence 68497 BP; 16500 A; 15015 C; 15455 G; 18939 T; 0 U; 2588 Other;

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Gaps
                                 0
 Length 68497;
                                 0; Indels
Score 14; DB 11; I
Pred. No. 5.6e+02;
0; Mismatches 0;
                                                                                                                                                    Search completed: May 16, 2005, 01:09:26 Job time : 210.25 secs
Query Match 87.5%; Scc
Best Local Similarity 100.0%; Pr
Matches 14; Conservative 0;
                                                                                                 43582 CTGCGTAGGCAATC 43595
                                                                  2 CTGCGTAGGCAATC 15
                                                                     ð
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Sequence 12683, A Sequence 13194, A Sequence 12287, A Sequence 14864, A Sequence 16001, A Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli

Sequence 2980, Ap Sequence 183, App Sequence 181, App Sequence 529, App Sequence 2, Appli Sequence 2, Appli

Seguence:

. 6

Run

Searched:

Database

Result

Sequence Sequence

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APPLICANT: Dillon, Patrick J.
APPLICANT: Choi, Gil H.
APPLICANT: Welch, Rodney A.
TITLE OF INVENTION: Nucleotide Sequence of Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90.0%; Score 14.4; DB 3; Length 746; 93.8%; Pred. No. 70; cive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/976,259
FILING DATE: Herewith
CLASSIFICATION: 536
PRICA PELICATION DATA:
APPLICATION NUMBER: US 60/031,626 AND US 60/061,953
ATTORNEY APPLICATION NUMBER: US 60/031,626 AND US 60/061,953
ATTORNEY AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 1488.0740002/EKS/CBM
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID No: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Sterne, Kessler, Goldstein & Fox P.L.L.C. 1100 New York Ave, N.W., Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20005-3334
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage COMPUTER: 419 Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
US-09-949-016-12683
US-09-949-016-13194
US-09-949-016-12287
US-09-949-016-1287
US-09-949-016-1287
US-09-198-452A-1
4 US-09-138-185A-1
3 US-09-103-840A-2
3 US-09-103-840A-1
US-09-603-208A-181
US-09-603-208A-181
US-09-603-208A-181
US-09-603-208A-181
US-09-603-208A-181
US-09-613-308A-181
US-09-613-008A-181
US-09-318-196G-5482
                                                                                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16, Application US/08976259
Patent No. 6316609
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 746 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                317366
1230025
1230230
4403765
4411529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No. 6316609
NUMBER OF SEQUENCES: 142
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Best Local Similarity 93.8'
Matches 15; Conservative
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1368
2715
5240
5240
25
                  152524
285986
288031
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ADDRESSEE: Sterne, Ke
STREET: 1100 New Yor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
   USA
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   STATE:
   Sequence 16, Appl
Sequence 16, Appl
Sequence 32451, A
Sequence 113217,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 331, App
Sequence 373, App
                                                                                                                            (without alignments)
437.251 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                             May 16, 2005, 00:11:05 ; Search time 59.875 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-513-999C-32451
US-09-949-016-113217
US-09-107-433-331
US-08-543-681A-2589
US-09-544-38-27
US-09-564-318-27
US-09-954-314-27
US-08-050-132A-1
US-08-750-222A-1
US-08-750-222A-1
US-08-815-652B-1
US-08-815-652B-1
US-08-254-333A-1
PCT-US92-05374A-1
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US-09-504-358-16
US-09-954-314-16
US-10-230-562-16
US-09-949-016-16210
US-09-960-3
                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                         1202784 seqs, 818138359 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                           OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                           IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                           tctgcgtaggcaatcc 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patents NA:*
                                                                                                                                                                     US-10-808-187A-2473
16
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Maximum DB seq length: 200000000
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Gaps

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1 TCTGCGTAGGCAATCC 16

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Sequence

US-09-543-771B-9 US-09-949-016-14199

72049

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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Patrick J. Dillon et al.

TITLE OF INVENTION: Nucleotide Sequences of Escherichia coli Pathogenicity Islands;
FILE REFERENCE: PB32401

CURRENT APPLICATION NUMBER: US/09/956,004

CURRENT APPLICATION NUMBER: US/09/920

PRIOR APPLICATION NUMBER: 08/976,259

PRIOR APPLICATION NUMBER: 06/061,953

PRIOR FILING DATE: 1997-11-21

PRIOR FILING DATE: 1997-11-22

PRIOR FILING DATE: 1997-11-23

PRIOR FILING DATE: 1997-11-23

SOFTWARE: PACENTION NUMBER: 06/031,626

NUMBER OF SEQ ID NOS: 142

SOFTWARE: PACENTIN VERSION 3.1

SEQ ID NO 16

LENGTH: 746

TYPE: DNA

CRANISM: Escherichia coli
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NAME/KEY: misc feature

LOCATION: (718)..(718)

OTHER INFORMATION: n equals a, t, g, or

NAME/KEY: misc feature

LOCATION: (741)..(741)

GOTHER INFORMATION: n equals a, t, g, or

US-09-956-004-16
                                                                                                                                                                                                                              Sequence 16, Application US/09956004
Patent No. 6787643
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334 TCTGCGTAGCCAATCC 319
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SOFTWARE: Patent.pm
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CRGANISM: Homo sapiens
US-09-513-999C-32451
                                                                                                                                                                                      US-09-956-004-16/c
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LENGTH: 470
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FOR DIAGNO
                                                             GENERAL NO. GENERAL S. GENERAL S. GENERAL GF. INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; FILE REFERENCE: CL001307; CURRENT APPLICATION NUMBER: 60/29/949,016; CURRENT FILING DATE: 2000-04-14; PRIOR APPLICATION NUMBER: 60/231,768; PRIOR APPLICATION NUMBER: 60/231,768; PRIOR PRIOR DATE: 2000-10-03; PRIOR PRIUR DATE: 2000-00-03; PRIOR FILING DATE: 2000-09-08; NUMBER OF SEQ ID NOS: 207012; SOFTWARE: FastsEQ for Windows Version 4.0; SEQ ID NO 113217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    itent No. 6800/4*
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David bull:
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      83.8%; Score 13.4; DB 4; Length 601; 93.3%; Pred. No. 2.7e+02; ive 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 5206
CORRESPONDENCE ADDRESSE:
ADDRESSEE: GENOME THERAPEUTICS CORPORATION
STREET: 100 Beaver Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
FILING DATE: 30-Jun-1998
APPLICATION DATA:
APPLICATION NUMBER: 60/085131
FILING DATE: May 12, 1998
FILING DATE: July 2, 1998
FILING DATE: July 2, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ariniello, Pamela Deneke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: «Unknown»
OPERATING SYSTEM: «Unknown»
SOFTWARE: «Unknown»
CURRENT APPLICATION DATA:
                 Sequence 113217, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 331, Application US/09107433
Patent No. 6800744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (781)893-50
TELEFAX: (781)893-8277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Waltham
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           149 rcrácaraddchárc 135
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Best Local Similarity 93.3'
Matches 14; Conservative
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US-09-949-016-113217/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-949-016-113217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Human'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 5
US-09-107-433-331/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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Gaps

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                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mohr, Christine
APPLICANT: Mohr, Christine
APPLICANT: Mendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
ITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
ITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES:
ADDRESSEE: NO. 62220.
                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                       Query Match 83.8%; Score 13.4; DB 4; Length 669; Best Local Similarity 93.3%; Pred. No. 2.8e+02; Matches 14; Conservative 0; Mismatches 1; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416 FILING DATE: 24-DEC-1997 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: CH 0016/97 FILING DATE: 31-DEC-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEPHONE: 919-541-8689
INFORMATION FOR SEQ ID NO: 373:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                               ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                         , NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...669
; SEQUENCE DESCRIPTION: SEQ ID NO: 331:
US-09-107-433-331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 373, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina COUNTRY: USA
                                                                                                       TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
INFORMATION FOR SEQ ID NO: 331:
SEQUENCE CHARACTERISTICS:
LENGTH: 669 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CTGCGTAGGCAATCC 16
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JS-08-998-416-373/c
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Sequence 2589, Application US/09543681A
Patent No. 6665709
GENERAL INFORMATION:
APPLICANT: GARY BRETON
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNCE: 2709.1002-001
CURRENT FILING DATE: 2009-04-05
PRIOR APPLICATION NUMBER: US 60/128,706
PRIOR FILING DATE: 1999-04-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INCORMATION:
APPLICANT: ROUVidere, Pierre E.
APPLICANT: ROUVidere, Pierre E.
APPLICANT: Brostowicz, Patricia C.
TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIATE FILE REFERENCE: BC1001 US NA
CURRENT APPLICATION NUMBER: 105/9/504,358
CURRENT FILING DATE: 2000-02-15
BARLIER FILING DATE: 1999-February-19
NUMBER OF SEC ID NOS: 49
SOFTWARE: Microsoft Office 97
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                                                                                                                                               1; Indels
                                                                                                     Score 13.4; DB 3;
Pred. No. 2.8e+02;
0; Mismatches 1;
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Pred. No. 3.2e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 27, Application US/09504358
; Patent No. 6365376
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CRGANISM: Brevibacterium sp HCU
US-09-504-358-27
    DNA (genomic)
                                                                                                       83.8%;
93.3%;
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                                                                                                                                                                                                                       425 CTGCGTTGGCAATCC 411
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Proteus mirabilis
US-09-543-681A-2589
                                                                                                                                               14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14; Conservative
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Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 8344
SEQ ID NO 2589
; MOLECULE TYPE: DNA (Ge
; ORIGINAL SOURCE:
; ORGANISM: PAG1284UP
US-08-998-416-373
                                                                                                     Query Match
Best Local Similarity
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Best Local Similarity
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Gaps
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ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLICATION NUMBER: US/08/050,132A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-08-750-222A-1/C
Sequence 1, Application US/08750222A
Fatent No. 6034061
GENERAL INFORMATION:
APPLICANT: Rosen, Vicki A.
APPLICANT: Rosen, Vicki A.
APPLICANT: Celeste, Anthony J.
APPLICANT: Song, Jeffrey
APPLICANT: Thies Socit
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 19
                                                         ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 51:
TELECOMMUNICATION INFORMATION:
TELEFAX: (617) 876-1170
TELEFAX: (617) 876-1170
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMMEDIATE SOURCE:
LIBRARY: Mouse liver cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              812 creceraceaaarce 798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
STRAIN: C57846xCBA
TISSUE TYPE: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 2447 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 83.8
Best Local Similarity 93.3
Matches 14; Conservative
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LOCATION: 1564..1893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
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POSITION IN GENOME:
Cambridge
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FEATURE:
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US-08-050-132A-1
                                             COUNTRY:
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                        Sequence 27, Application US/09954314

Pacent No. 646524

GRERAL INFORMATION:
GRESCOMICANT: ROUVIETE, Pierre E.
APPLICANT: ROUVIETE, Pierre E.
TITLE OF INVENTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID INTERMEDIATES
FILE REPERENCE: BC1001 US NA
CURRENT APPLICATION NUMBER: US/09/954,314

CURRENT APPLICATION NUMBER: US/09/954,314

PRIOR PELING DATE: 1999-February-19
NUMBER OF SEQ ID NOS: 49

SOFTWARE: Microsoft Office 97

LENGTH: 2200
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Batent No. 6790645

GENERAL INFORMATION:
APPLICANT: ROUVIÈTE, Pierre E
APPLICANT: Brzostowicz, Patricia C
APPLICANTION: GENES AND ENZYMES FOR THE PRODUCTION OF ADIPIC ACID
TITLE OF INVENTION: INTERMEDIATES
FILE REPERBNCE: BC-1001
CURRENT APPLICATION NUMBER: US/10/230,562
CURRENT FILING DATE: 2002-08-29
PRIOR FILING DATE: 1999-02-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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83.8%; Score 13.4; DB 4; Length 2200;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
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STREET: Legal Affairs - 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wozney, John M.
APPLICANT: Wezney, John M.
APPLICANT: Celeste, Anthony
TITLE OF INVENTION: BMP-9 COMPOSITIONS
TOWNER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-08-050-132A-1/c
; Sequence 1, Application US/08050132A
; Patent No. 5661007
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Brevibacterium sp HCU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Brevibacterium sp HCU
US-10-230-562-27
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SOFTWARE: Microsoft Office 97
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Matches 14; Conservative
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LENGTH: 2200
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US-10-230-562-27
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                     US-09-954-314-27
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                                                                                          ZIP: 02140

MEDIUM TYPE: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
GOTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/815,652B
FILING DATE:
                STREET: Legal Affairs - 87 CambridgePark Drive CITY: Cambridge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

83.8%; Score 13.4; DB 3;
Best Local Similarity 93.3%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rosen, Vicki A.
APPLICANT: Wozney, John M.
APPLICANT: Celeste, Anthony J.
APPLICANT: Song, Jeffrey
APPLICANT: Thies, Scott
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                               CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: KAPINOS, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 5186D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
  Genetics Institute, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-254-353A-1/c

Sequence 1, Application US/08254353A

Patent No. 6287816

GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mouse liver cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       812 creceraecaaarce 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Mus musculus
STRAIN: C57B46xCBA
TISSUE TYPE: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: mat_peptide
LOCATION: 1564..1893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
610..1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY: Mouse liv
CLONE: ML14A
POSITION IN GENOME:
UNITS: bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL: N
ANTI-SENSE: NO
                                                                            as
ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY:
; LOCATION:
US-08-815-652B-1
                                                       STATE: N
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Indels
                                                               COMPUTE: NEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BEN FC COMPATISH
COMPUTER: PEN FC COMPATISH
COMPUTER: PEN FC FOSTMS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NUMBER: US/08/750,222A
FILING DATE: 04-DEC-1996
CLASSIFICATION DATA:
RAPPLICATION DATA:
APPLICATION NUMBER: 08/254,353
FILING DATE:
ATTOMARY NUMBER: 08/254,353
FILING DATE:
ATTOMARY NUMBER: 08/254,353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                       NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 5186B
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 876-1170
TELEFAX: (617) 876-5891
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mozney, John M.
APPLICANT: Celeste, Anthony
APPLICANT: Song, Jeffrey
APPLICANT: Thies, R. Scott
TITLE OF INVENTION: BMP-9 COMPOSITIONS
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08815652B
Patent No. 6034062
GENERAL INFORMATION:
APPLICANT: Wozney, John M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: MUS MUSCULUS STRAIN: C57B46xCBA TISSUE TYPE: liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IMMEDIATE SOURCE:
LIBRARY: Mouse liver cDNA
CLONE: ML14A
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             812 CTGCGTAGGAAATCC 798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2447 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 83.8
Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: mat_peptide
LOCATION: 1564..1893
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610..1896
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1..2447
Cambridge
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US-08-815-652B-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
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US-08-750-222A-1
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                                     COUNTRY:
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Gaps

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Search completed: May 16, 2005, 06:11:37 Job time : 66.875 secs
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application PC/TUS9205374A
GENERAL INFORMATION:
APPLICANT: Wozney, John M.
ITTLE OF INVENTION: BMP-9 COMPOSITIONS
ITTLE OF INVENTION: BMP-9 COMPOSITIONS
CORRESPONDENCE ADDRESS: 9
CORRESPONDENCE ADDRESS: 7
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
STATE: MA
ADDRESSEE: Genetics Institute, Inc.
STREET: Legal Affairs - 87 CambridgePark Drive
CITY: Cambridge
                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/254,353A
                                                                                                                                                                                                                                       APPLICATION ...

FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REFERENCE/DOCKET NUMBER: GI 5186B
TELECOMMUNICATION INFORMATION:
FELEPHONE: (617) 876-5851
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2447 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
TOPOLOGY: linear
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: CDNA to mENA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Mus musculus
STRAIN: C57846xCBA
TISSUE TYPE: liver
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            812 creceraceaaarce 798
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NAME/KEY: mat_peptide
LOCATION: 1564..1893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDS
610..1896
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POSITION IN GENOME:
UNITS: bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCT-US92-05374A-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
LOCATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
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LOCATION:
US-08-254-353A-1
                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
MEDIUM TYPE: FLOPPY GLER.

COMPUTER: IBM FC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOCTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/05374A
FILING DATE: 19920625

CLASSIFICATION: PORMATION:
NAMME: Kapinos, Ellen J.
REGISTRATION NUMBER: 32,245
REGISTRATION NUMBER: 31,245
REGISTRATION POR PROPERTION:
TELEPHONE: (617) 876-1170
TELEPHONE: (617) 876-1170
TELEPHONE: 417 base pairs
TELEPHONE: 2447 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 13.4; DB 5;
Pred. No. 3.3e+02;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 93.3%;
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  812 CTGCGTAGGAAATCC 798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIBRARY: Mouse liver cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 CTGCGTAGGCAATCC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNITS: bp
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 1564..1893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
610..1896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN: C57B46xCBA
TISSUE TYPE: liver
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: mRNA
LOCATION: 1..2447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLONE: ML14A
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     , LOCATION:
PCT-US92-05374A-1
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May 16, 2005, 02:00:36; Search time 788.5 Seconds (without alignments) 129:102 Million cell updates/sec
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17: /cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5662332 segs, 3060109652 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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16
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	473, Ap	 Appli 	1, Appl	, Appli	5, Appl	, Appli	7 - 1				
Description	Sequence 2473, Ap	Sequence 1	Sequence 1	Sednence 9	Sequence 5	Seguence 6	Sequence 4	Sequence 7	Sequence 1	Sequence 1	11111
ΩI	US-10-808-187-2473	US-10-808-187-1	US-10-808-187-11	US-10-699-936-9	US-10-889-447-5	US-10-889-447-6	US-10-889-447-4	US-10-889-447-7	US-10-839-729-15	US-10-827-757-1	0 117 000 01 011
	19	19	19	19	19	19	19	19	18	18	•
% Query Match Length DB	16	646	1213	5262	28920	28920	29291	29430	29727	29727	000
% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	000
Score	16	16	16	16	16	16	16	16	16	16	,
Result No.	1	~	e	4	2	9	7	ω	σ	70	;
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•	US-TO-639-336-T	-67/-660	0-889-44	10-699	US-10-839-729-16	-18	US-10-808-187-16	w	0-808-18	US-10-808-187-1108	10-808-18	US-10-808-187-1965	US-10-889-447-10	US-10-839-729-14	US-10-856-529-1	US-10-626-879-67	US-10-889-447-1	US-10-889-447-2	US-10-699-936-2	US-09-956-004-16	US-10-808-570-16	US-09-938-842A-1164	US-09-938-842A-1164	US-10-437-963-27078	US-10-743-884-11	US-10-744-150-9	US-09-880-107-2145	US-10-425-115-25291	US-10-425-115-87839	0-425-11	-10-425-1	-10-425-115-	-10-425-115-87	US-10-425-115-87810
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7	97.	9 1	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	16	14.4	14.4	14.4	4	14.4	14.4	4	4	14	14	14	14	14	14	14
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ALIGNMENTS

US-10-808-187-2473
; Sequence 2473, Application US/10808187
; Publication No. US20050009009A1
; GENERAL INFORMATION:
APPLICANT: PEIRIS, JOSEPH S. M.
APPLICANT: POON, LIT NAM
APPLICANT: GUAN, KWCK YUNG
APPLICANT: GUAN, KWCK HUNG
TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
TITLE OF INVENTION: RESPIRATORY SYNDROME (SARS)
FILE REFRENCE: V9661.078
FRICH RAPPLICATION NUMBER: 00/457,031
FRICH RAPPLICATION NUMBER: 00/459,931
FRICH RAPLICATION NUMBER: 60/459,931
FRICH RILING DATE: 2003-04-06
FRICH RILING DATE: 2003-04-06
FRICH FILING DATE: 2003-04-08
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FRICH RILING DATE: 2003-04-14
FRICH RILING DATE: 2003-04-13
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FRICH RILING DATE: 2003-04-14
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FRICH RILING DATE: 2003-04-13

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TYPE: DNA
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APPLICANT: YUEN, KWOK YING
APPLICANT: GUAN, YI
APPLICANT: HING
APPLICANT: HING
APPLICANT: AICHOLLS, JOHN
TITLE OF INVENTION: RESPIRATORY SYNDROME (SARS)
FILE REFERENCE: V9661.0078
CURRENT PILING DATE: 2004-03-24
FRIOR APPLICATION NUMBER: 60/457, 031
FRIOR APPLICATION NUMBER: 60/457, 730
FRIOR PELLING DATE: 2003-03-26
FRIOR PELLING DATE: 2003-04-03
FRIOR PILING DATE: 2003-04-03
FRIOR FILING DATE: 2003-04-03
FRIOR PILING DATE: 2003-04-03
FRIOR PELLING DATE: 2003-04-03
FRIOR FILING DATE: 2003-05-05
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                                                                                                                                                                                                                                          ; OTHER INFORMATION: Description of Artificial Sequence: Probe US-10-808-187-2473
                                                                                                                                                                                                                                                                                                                                                100.0%; Score 16; DB 19; Length 16; 100.0%; Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/10808187
Publication No. US200500090091
GENERAL INFORMATION
APPLICANT: PEIRIS, JOSEPH S. M.
APPLICANT: YUEN, KWOK YUNG
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Best Local Similarity 100.0%;
Matches 16; Conservative (
                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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NUMBER OF SEQ ID NOS: 2476
SOFTWARE: PatentIn ver. 3.2
SEQ ID NO 2473
LENGTH: 16
                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
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US-10-808-187-1
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US-10-808-187-1/c
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APPLICANT: CHAN, KWOK HUNG
APPLICANT: GUAN, YI
APPLICANT: CHAN, KWOK HUNG
APPLICANT: CHAN, KWOK HUNG
APPLICANT: CHAN, KWOK HUNG
TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
TITLE OF INVENTION: RESPIRATORY SYNDROME (SARS)
FILE REFERENCE: V9661.0078
CURRENT APPLICATION NUMBER: US/10/808,187
CURRENT APPLICATION NUMBER: 60/457,031
PRIOR APPLICATION NUMBER: 60/457,730
PRIOR APPLICATION NUMBER: 60/459,931
PRIOR PILING DATE: 2003-04-03
PRIOR APPLICATION NUMBER: 60/460,357
PRIOR APPLICATION NUMBER: 60/460,357
PRIOR APPLICATION NUMBER: 60/460,357
PRIOR APPLICATION NUMBER: 60/461,265
PRIOR PILING DATE: 2003-04-08
PRIOR PILING DATE: 2003-04-23
PRIOR PILING DATE: 2003-04-23
PRIOR PILING DATE: 2003-04-23
PRIOR FILING DATE: 2003-04-23
PRIOR FILING DATE: 2003-05-05
PRIOR PRIOR FILING DATE: 2003-05-05
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PRIOR PR
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Sequence 9, Application US/1069936
Publication No. US20050095582A1
GENERAL INFORMATION:
APPLICANT: Gillim-Ross, Laura
APPLICANT: Taylor, Jill
APPLICANT: Scholl, David R.
APPLICANT: Scholl, David R.
APPLICANT: Wentworth, David E.
APPLICANT: Wentworth, David E.
APPLICANT: Wentworth, David E.
APPLICANT: Wentworth, Scholl, David E.
APPLICANT: Wentworth, David E.
APPLICANT: Wentworth, David E.
APPLICANT: Wentworth, David E.
APPLICANT: Wentworth, John Compositions and Methods for Detecting Severe Acute Respiratory
TITLE OF INVENTION: Syndrome Coronavirus
FILE OF INVENTION: Syndrome Coronavirus
CURRENT APPLICATION NUMBER: US/10/699,936
CURRENT FILING DAVIS: 2003-11-03
NUMBER OF SEQ ID NOS: 87
SOFTWARE: PatentIn version 3.2
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100.0%; Pred. No. 18;
cive 0; Mismatches 0;
Sequence 11, Application US/10808187
Publication No. US200500090091
GENERAL INFORMATION:
APPLICANT: PEIRIS, JOSEPH S. M.
APPLICANT: YUEN, KWOK YUNG
APPLICANT: POON, LIT MAN
APPLICANT: GUAN, YI
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SOFTWARE: Patentin ver. 3.2
SEQ ID NO 11
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Matches 16; Conservative
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US-10-808-187-11
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US-10-699-936-9/c
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LENGTH: 5262
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Gaps
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CURRENT FILING DATE: 2004-07-12

PRIOR PRILING DATE: 2003-07-12

NUMBER OF SEQ ID NOS: 241

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 29291
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TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N. EXPRESSION
FILE REFERENCE: RIS-0685US
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Best Local Similarity 100.0%; Pred. No. 22;
Matches 16; Conservative 0; Mismatches 0;
                                Mismatches
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             Pred. No.
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CURRENT FILING DATE: 2004-07-12
PRIOR APPLICATION NUMBER: 60/486,670
PRIOR FILING DATE: 2003-07-12
NUMBER OF SEQ ID NOS: 241
SOFTWARE: FastSEQ for Windows Version 4.0
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ORGANISM: SARS coronavirus isolate BJ02
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100.0%; Pr
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Publication No. US20050075307A1
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/10889447; Publication No. US20050075307A1; GENERAL INFORMATION:
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APPLICANT: Jain, Ravi
                                Conservative
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Matches 16; Conservative
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Matches 16; Conserva
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100.0%; Score 16; DB 19; Length 28920;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 16; Conservative 0; Mismatches 0; Indels 0;
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                                                                                        19; Length 5262;
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TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
FILE REFERENCE: RTS-0685US
CURRENT APPLICATION NUMBER: US/10/889,447
CURRENT FILING DATE: 2004-07-12
PRIOR PRILING DATE: 2003-07-12
NUMBER OF SEQ ID NOS: 241
SOFTWARE: FASESEQ for Windows Version 4.0
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TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
FILE REPERENCE: RTS-0685US
CURRENT APPLICATION NUMBER: US/10/889,447
CURRENT FILING DATE: 2004-07-12
PRIOR APPLICATION NUMBER: 60/486,670
PRIOR APPLICATION NUMBER: 60/486,670
PRIOR APPLICATION NUMBER: 231
NUMBER OF SEQ ID MOS: 241
SOFTWARE: FASTESQ for Windows Version 4.0
                                                                                                                                  0; Indels
                                                                                        100.0%; Score 16; DB 100.0%; Pred. No. 20;
                                                                                                                                  Mismatches
    ; TYPE: DNA
; ORGANISM: SARS coronavirus Shanghai QXC
US-10-699-936-9
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ORGANISM: SARS coronavirus isolate BJ04
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Publication No. US20050075307A1
GENERAL INFORMATION:
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Publication No. US20050075307A1
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
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                                                                              Query Match
Best Local Similarity 100.0
Matches 16; Conservative
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APPLICANT: Jain. Re
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SEQ ID NO 5
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LENGTH: 28920
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US-10-889-447-5/c
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US-10-889-447-6/c
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APPLICANT: Gillim-Ross, Laura
APPLICANT: Gillim-Ross, Laura
APPLICANT: Taylor, Jill
APPLICANT: Scholl, David R.
APPLICANT: Scholl, David R.
APPLICANT: Wentworth, David E.
APPLICANT: Jollick, Joseph D.
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
TITLE OF INVENTION: Syndrome Coronavirus
FILE REFERENCE: DHI-07986
CURRENT APPLICATION NUMBER: US/10/699,936
CURRENT FILING DATE: 2003-11-03
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.2
SEQ ID NO 1
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Publication No. US20050002953A1
GENERAL INFORMATION: US20050002953A1
TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
TITLE OF INVENTION: AND METHODS OF USE
FILE REPERENCE: BIOBANK.013A
CURRENT APPLICATION NUMBER: US/10/839,729
CURRENT PLING DATE: 2004-05-04
PRIOR PILING DATE: 2003-05-06
                                                                                                                                                                                                                                                                                        Score 16; DB 19;
Pred. No. 22;
; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/10/889,447
CURRENT FILING DATE: 2004-07-12
PRIOR APPLICATION NUMBER: 60/486,670
PRIOR FILING DATE: 2003-07-12
NUMBER OF SEQ ID NOS: 241
SOFTWARE: PARLSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 29727
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 29736
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US-10-699-936-1
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US-10-889-447-8
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Best Local Similarity 100.0%;
Matches 16; Conservative 0
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; ORGANISM: SARS Coronavirus
US-10-839-729-17
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US-10-839-729-17/c
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Sequence 1, Application US/1082757

Publication No. US20050004071A1

GENERAL INFORMATION:
APPLICANT: Comper, Wayne

TITLE OF INVENTION: Charged Polysaccharides Resistant To Lysosomal Degradation During

TITLE OF INVENTION: Kidney Filtration And Renal Passage And Their Use To Treat Or
TITLE OF INVENTION: Prevent Infection By Coronaviruses

FILE REFERENCE: 11213-007-999

CURRENT FILING DATE: 2004-04-20

PRIOR APPLICATION NUMBER: 60/464,294

PRIOR APPLICATION NUMBER: 60/464,294

PRIOR APPLICATION SEQ ID NOS: 1

NUMBER OF SEQ ID NOS: 1
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Publication No. US20050075307A1
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Jain, Ravi
ITILE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
FILE REFERENCE: RTS-0685US
                                                                                                                                                        GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Jens Harold
TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: BIOBANK: 013A
CURRENT APPLICATION NUMBER: US/10/839,729
CURRENT FILING DATE: 2004-05-04
PRIOR APPLICATION NUMBER: 60/468703
PRIOR PILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 29727
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ORGANISM: SARS-related coronavirus (Urbani strain)
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, Publication No. US20050002953A1
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Matches 16; Conservative
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LENGTH: 29727
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US-10-827-757-1/c
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APPLICANT: Gillim-Ross, Laura
APPLICANT: Taylor, Jill
APPLICANT: Taylor, Jill
APPLICANT: Scholl, David R.
APPLICANT: Wentworth, David E.
APPLICANT: Wentworth, David E.
APPLICANT: Jollick, Joseph D.
TITLE OF INVENTION: Syndrome Coronavirus
FILE REFERENCE: DHI-07986
CURRENT APPLICATION NUMBER: US/10/699,936
CURRENT PILING DATE: 2003-11-03
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.2
SEQ ID NO 3
LENGTH: 29736
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Pred. No. 22;
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                                                                                                                                                                                                                                                                                                        APPLICANT: Jain, Ravi
APPLICANT: Jain, Ravi
APPLICANT: Jain, Ravi
TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
FILE REFERENCE: RTS-0685US
CURRENT APPLICATION NUMBER: US/10/889,447
CURRENT FILING DATE: 2004-07-12
PRIOR RPLICHGO DATE: 2003-07-12
NUMBER OF SEQ ID NOS: 241
SOFTWARE: FRASER for Windows Version 4.0
SEQ ID NO 9
LENGTH: 29736
                                                  0; Indels
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CORGANISM: SARS coronavirus CUHK-W1
US-10-889-447-9
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Publication No. US20050075307A1
GENERAL INFORMATION:
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Publication No. US20050095582A1
GENERAL INFORMATION:
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Query Match
Best Local Similarity 100.0%;
Matches 16; Conservative 0
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Best Local Similarity 100.
Matches 16; Conservative
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US-10-699-936-3/c
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CC212165 1127 bp DNA linear GSS 12-WAY-2003 CH261-35M21_RM1.1 CH261 Gallus gallus genomic clone CH261-35M21, genomic survey sequence.
CC212165
BF323646 ShEST4a17
BIS98596 479571 MA
BF5.036 UT-H-BI4-
AA580065 n179g01.8
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BM176303 TGEST2215
CF248067 TGEST2215
BH518447 BCCCQQTF
AZ61985 1MA62ZN17
AZ61985 1MA62ZN17
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BP356568 BP356568
CB382455 TGESTZY97
BJ314417 BJ314417
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 1127)
Kremitzki,C., Higginbotham,J., Wylie,K., Carter,J., McPh
Warren,W., Garves,T., Mardis,E. and Wilson,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Washington University School of Medicine Email: submissions@watson.wustl.edu Insert Length: 182000 Std Brror: 0.00 Seg primer: RNI TACGACTCACTATAGGGAGA Class: BAC ends High quality sequence start: 113 High quality sequence stop: 766.
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/clone_lib="CH261"
                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
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/organism="Gallus gallus"
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/strain="Red_Jungle_Fowl"
/db_xref="taxon:9031"
/clone="CH261-35M21"
                                                         AZ836547
CN198330
BQ10303
BM176303
CF248067
CF247007
BH519859
BP276538
BP276538
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CH382556
                               BF510336
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Contact: Richard K. Wilson
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Gallus gallus
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CC212165/c
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KEYWORDS
SOURCE
ORGANISM
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DEFINITION
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COMMENT
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BU309142 603538844
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K-EST0184
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                                                                                               00:01:20 ; Search time 1807 Seconds (without alignments) 337.038 Million cell updates/sec
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CA833034
CC821220
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AV810831
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AW974032
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                5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                              34239544 seqs, 19032134700 residues
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                  GenCore version
Copyright (c) 1993 - 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
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Maximum Match 100%
Listing first 45 summaries
                                                                       OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                       1 tctgcgtaggcaatcc 16
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16
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Maximum DB seq length: 200000000
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Match Length DB
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gb_htc:*
gb_est3:*
gb_est4:*
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gb_est6:*
gb_gss1:*
gb_gss2:*
                                                                                                     May 16, 2005,
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BU309142/c DEFINITION KEYWORDS SOURCE ORGANISM

ACCESSION

VERSION

REFERENCE AUTHORS

MEDLINE PUBMED COMMENT

JOURNAL

TITLE

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/dev stage="1">
/ dev stage="1">
/ dev stage="1">
/ dev stage="1">
/ dev stage="1">
/ done lib="Poplar cDNA library from mature xylem"
/ done lib="Poplar cDNA library was made with mRNA isolated from opposite and tension wood tissues corresponding to the mature xylem collected after debarking the stem and pealing the young differentiating xylem with a scalpel. These tissues were collected on 3 different tilted trees grown in the nursery. cDNAs were closed in an oriented way into Sfil (A and B) restriction sites. A one-step conversion of Lambda TriplEx2 to the corresponding pTriplEx2 plasmid was done via site-specific recombination at loxp sites (Clontech, SWART CDNA library construction kit). CDNA inserts were PCR amplified using prings pringers and then sequenced on a ABI3100 Genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CF588852 379 bp mRNA linear EST 05-AUG-2004
DSS37 Coffee SSH library 1 Coffea arabica cDNA clone 12H9/52, mRNA
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Coffea arabica
Coffea arabica
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spernatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                          Populus alba x Populus tremula
Populus alba x Populus tremula
Bukaryota; Viridiplantae Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
I (bases 1 to 145)
Dejardin,A., Leple,J.-C., Lesage-Descauses,M.-C., Costa,G. and
Pilate,G.
                                                                                                                                                                                                                                                                                                          Expressed sequence tags from poplar wood tissues - A comparative analysis from multiple libraries Plant Biol. 6 (1), 55-64 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue type="mature xylem harvested on opposite and tension wood stem"
                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Leple JC
Unit of Forest improvement, Genetics and Physiology
Unit of Forest improvement, Genetics and Physiology
National Institute for Agricultural Research (INRA)
Domaine de Limere, BP20619 ARDON, 45166 OLIVET CEDEX, FRANCE
Tel: 33 02 38 41 78 00
Exax: 33 02 38 41 78 79
Email: Jean-Charles.Leple@orleans.inra.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         organism="Populus alba x Populus tremula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FORWARD: TriplexA 5' CTCGGGAAGCGCCCCATTGTG 3'
BACKWARD: TriplexB15' ATACGACTCACTATAGGGCGA 3'
Plate: PtaXM0017 row: E column: 7
Seg primer: TriplexA 5' CTCGGGAAGCGCGCCATTGTG 3'
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100.0%; Pred. No. 6.2e+02;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
/strain="clone 717-1-84"
/db_xref="taxon:80863"
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                             GI:33448231
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CF588852
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                                                                                                                                                                                                                                                        AUTHORS
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/lab_host="adult"
/lab_host="adult"
/lab_host="DH10B"
/cloon lib="CSEQCHN60"
/note="Organ: heart; Vector: pBluescript II KS(+); Site_1:
EcoRI, Site_2: Not1; This normalized library was
Constructed_from 1 million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
EcoNI, size-selected, and cloned into the NoI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soarse et al., pNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                               Gallus gallus (chicken)
Gallus gallus (alicken)
Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves;
Phasianinae; Gallus.
I (bases 1 to 1129)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A. Comprehensive Collection of Chicken CDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
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                                                                                                                                                                       BU309142 1129 bp mRNA linear EST 28-NOV-2002 603538844F1 CSEQCHN60 Gallus gallus cDNA clone ChESTS04h11 5', mRNA
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University of Manchester Institute of Science and Technology
(UMIST)
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/mol_type="mRNA"
/strain="Compton Line 151"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PO Box 88, Manchester, M60 1QD, UK Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9031"
/clone="ChEST504h11"
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/sex="Female"
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/lab host="E.coli"
/clone lib="Coffee SSH library 1"
/clone lib="Coffee SSH library 1"
/clone lib="Coffee SSH library 1"
/clone lib="Coffee SSH library 2"
/clone lib="Coffee SSH library 3"
/clone lib-"Coffee SSH library 3"
/clone SSH subtraction library 3"
/clone SSH library 3"
/clone SSH library 4"
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1 (bases 1 to 476)
Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
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K-EST0184175 L4SNU368s1 Homo sapiens CDNA clone L4SNU368s1-20-H07
                                                                                                                                                                                       Coffee (Coffee arabica L.) genes early expressed during infection by the rust fungus (Hemileia vastatrix)

by the rust fungus (Hemileia vastatrix)

by the rust fungus (Hemileia vastatrix)

Contact: Fernandez, D. (6) (2004) In press

Contact: Fernandez, D. (7)

Equipe Resistance des Plantes aux Parasites, UMR DGPC 1097

IRD

911, avenue Agropolis, BP64501,34394 Montpellier cedex 5, France

Tel: +33 467 416 283
asterids; lamiids; Gentianales; Rubiaceae; Ixoroideae; Coffeeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Differentially screened sequence (stronger hybridization signal with incompatible probe versus compatible probe). POIXVa=No.
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                                                                                                   Fernandez, D., Santos, P., Agostini, C., Bon, M.C., Petitot, A.S.,
Silva, M.C., Guerra-Guimaraes, L., Ribeiro, A., Argout, X. and
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Korea Research Institute of Bioscience & Biotechnology
52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
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Pred. No. 76+02;
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/organism="Coffea arabica"
/mol type="mRNA"
/cultivar="S4Agaro"
/db.xref="taxon:13443"
/clone="12H9/52"
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Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: Diana.Fernandez@mpl.ird.fr
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Email: yongsung@mail.kribb.re.kr
Plate: 20 row: Hoolumn: 07
High quality sequence stop: 476.
Location/Qualifiers
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100.0%; Prer
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                                                                      (bases 1 to 379)
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/call type="Liver"
/call line="SNU-368"
/lab hose="Polygonal"
/call line="SNU-368"
/lab hose="Polygona"
/coll line="SNU-368"
/clone libe="Liver; Vector: pCNS-D2; Site_l: EcoRI;
Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoRI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The GDNA vector was adjusted to have about 60nt. The GDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF' by electroporation method. The CDNA libraries constructed by this method are full-length enriched CDNA library. After analyzing and sequencing about 2.000 - 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including Ty promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of blotinylated single stranded RNA by in vitro transcription reaction. The synthesized NNA probes were hybridized with artisense single stranded CDNAs prepared from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted CDNA into competent cells E. coli ToplOF' with
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100.0%; Pred. No. 7.2e+02;
iive 0; Mismatches 0;
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Umea Plant Science Center
Department of Plant Physiology
University of Umea, 901 87 Umea, Sweden
clone="L4SNU368s1-20-H07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 electroporation method
                                                                               tissue type="Liver"
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BU819258
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Fortune tremula

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.

El (bases 1 to 609)

Sterky, F., Bhalbarao,R.R., Unneberg,P., Segerman,B., Nilsson,P.,

Brunner,A.M., Campaa,L., Jonsson-Lindvall,J., Tandre,K.,

Strauss,S.H., Sundberg,B., Gustafsson,P., Uhlen,M., Bhalerao,R.P.,

Nilsson,O., Sandberg,G., Karlsson,J., Lundeberg,J. and Jansson,S.

A Populus EST resource for functional genomics

Unpublished (2003)

Other ESTS: UA41BPP03. UA41BPP03.5pR

Contact: Bo Segerman

Umea Plant Science Center, Department of Plant Physiology

Umea University

901 87 Umea, Sweden

Tel: 446 90 786 5279

Fax: 446 90 786 5279
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                                                                                                                                                  CK096013 609 bp mRNA linear EST 01-DEC-2003 UA41BPF03.3pR Populus dormant cambium cDNA library Populus tremula cDNA clone UA41BPF03 3', mRNA sequence.
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Spermatophyta, Magnollophyta, eudicotyledons, core eudicots,
Caryophyllales, Alzoaceae, Mesembryanthemum.
I (bases 1 to 650)
Cushman, J.C.
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Contact: Cushman JC
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Pred. No. 7.5e+02;
0; Mismatches 0; Indels
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Mesembryanthemum crystallinum
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/mol_type="mRNA"
/db_xref="taxon:113636"
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100.0%; Pre
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/db_xref="taxon:3544"
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/draftasue_type="lasf"
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library, 0 hours NaCl_treatment_prescreened_for_removal_of
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MCA046F07_23578 Ice plant Lambda Uni-Zap XR expression library, 0 hours NaCI treatment prescreened for removal of highly abundant transcripts Mesembryanthemum crystallinum cDNA clone MCA046F07 5, BM302197
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Mesembryanthemum crystallinum (common iceplant)
Mesembryanthemum crystallinum
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Caryophyllales, Alzoaceae, Mesembryanthemum.
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An expressed sequence tag database for the common ice plant, Messembryanthemum crystallinum
Mupublishad (1997)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Fel: 775-784-1650
                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:113636"
/tiseue type="cambium"
/clone_lib="Populus tremula cambium cDNA library"
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                                                                                                                                                                                                                                                                      Length 557;

    .560
/organism="Mesembryanthemum crystallinum"

                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                      DB 5; Le
7.4e+02;
Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: rupali.bhalerac@plantphys.umu.se.
Location/Qualifiers
                                                                                                             /organism="Populus tremula"
                                                                                                                                                                                                                                                                    Ouery Match 93.8%; Score 15; DB Best Local Similarity 100.0%; Pred. No. 7.4 Matches 15; Conservative 0; Mismatches
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BACKWARD: T7 21mer
Place: 046 row. F column: 07
Seq primer: T3 20mer
High quality sequence stop: 560.
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TITLE
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Gaps

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us-10-808-187a-2473.rst

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CA836742 689 bp mRNA linear EST 12-DEC-2002 MCU010E08 256046 Ice plant Lambda Uni-Zap XR expression library, 5 days 0.5 M NaCl treatment, Crassulacean acid metabolism, phase II (8:00 AM). Mesembryanthemum crystallinum cDNA clone MCU010E08 5, CA836742
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/dev_stage="five-week-old"
/dev_stage="five-week-old"
/clone_lib=Tce plant Lambda Uni-Zap XR expression
library, 5 days 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase II (8:00 AM)."
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site 1:
EcoR]; Site_2: Xhol; Library construction was performed
according to Stratagene's recommended protocol for the
Lambda UniZapXR vector and cDNA synthesis kit."
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Aizoaceae; Mesembryanthemum.

1 (bases 1 to 689)
Cushman, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum
L Unpublished (1997)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1050
Email: jushman@unr.edu
PCR PRimers
FORWARD: T3 20mer
Plate: 010 row. E column: 08
Seq primer: T3 20mer
High quality sequence stop: 689.
                                                       Gaps
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                 Length 667;
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                                                       0; Indels
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Mesembryanthemum crystallinum
               Score 15; DB 9; Le
Pred. No. 7.6e+02;
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Pred. No. 7.6e+02;
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100.0%; Pred. No. .
0; Mismatches
                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
93.8%; Scc.
100.0%; Pre
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465 TCTGCGTAGGCAATC 479
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Best Local Similarity
               Query Match
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Matches 15; Conserv
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CA836742
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                               /tissue type="leaf"
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/dev stage="five-week-old"
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library, 5 days 0.5 M NaCl treatment, Crassulacean acid
metabolism, phase I (2 AM)."
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EcoRI; Site_2: XhoI; Library construction was performed
according to Stratagene's recommended protocol for the
Lambda UniZapXR vector and cDNA synthesis kit."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     vor up DNA linear GSS 22-OCT-200 GEOPOIC, genomic survey sequence.
CC821220
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0
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/organism="Mesembryanthemum crystallinum"
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Biology Dept.
San Diego State University
5500 Campanile Dr, San Diego, CA 92102, USA
Tel: 6195941336
Fax: 619595676
Email: forest@sunstroke.sdsu.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93.8%; Score 15; DB 6; Le
100.0%; Pred. No. 7.5e+02;
iive 0; Mismatches 0;
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                                                                                                                                                FORWARD: T3 20mer
BACKWARD: T7 21mer
Plate: 019 row. C column: 05
Seq primer: T3 20mer
High quality sequence stop: 650.
    Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
Email: joushman@unr.edu
PCR PRimers
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uncultured human fecal virus
Viruses; environmental samples.
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Best Local Similarity 100.*
Matches 15; Conservative
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CC821220
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Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chout, Tsurumi-tut, Yokohama, Kanagawa 230-0045, Japan (B-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-911, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan Phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST 07-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mesembryanthemum crystallinum (common iceplant)
Mesembryanthemum crystallinum
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Caryophylales; Aizoaceae; Mesembryanthemum.

1 (bases 1 to 774)
Bohnert, H.J., Borchert, C., Brazille, S., Brooks, J., Eaton, M.,
Ferrea, H., Kawasaki, S., McCollough, A., Michalowski, C.B.,
Palacio, C., Scara, G., Mheeler, M. and Zepeda, G.R.
Functional Genomics of Plant Stress Tolerance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue type="mixture of kidney and spleen"
/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.8%; Score 15; DB 9; Length 726; 100.0%; Pred. No. 7.7e+02; ive 0; Mismatches 0; Indels
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Bio Sciences West room 513, Tucson, AZ 85721, USA
Bio Sciences West room 513, Tucson, AZ 85721, USA
Fax: 520-621-1697
Email: cbm@u.arizona.edu
An open reading frame exists.
Insert Length: 1 Std Error: 0.00.
Location/Qualifiers
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/clone="MSMG01-317M24.TJ"
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/db_xref="taxon:3544"
/tissue_type="roots"
/dev_stage="5-6 weeks"
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100.0%; Fi
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Contact: Michalowski, C.B.
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                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Bepermatophyta; Bepermatophyta; Bepermatophyta; Care eudicots; Caryophyllales; Aizoaceae; Mesembryanthemum.

(bases 1 to 697)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
            8:00 AM). Mesembryanthemum crystallinum cDNA clone MCU003H04 5,
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An expressed sequence tag database for the common ice plant,
Mesembryanthemum crystallinum
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BAC end Sequences of Library MSMg01
Unpublished
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Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
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                                                                                                            Mesembryanthemum crystallinum (common iceplant)
Mesembryanthemum crystallinum
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                                                                                                                                                                                                                                                                                             Unpublished (1997)
Contact: Cushman JC
Department of Biochemistry
University of Nevada
MS200, Reno, NV 89557-0014, USA
Tel: 775-784-1918
Fax: 775-784-1650
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Seg primer: T3 20mer
High quality sequence stop: 697.
Location/Qualiflers
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Mus musculus molossinus
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AG437780.1 GI:48080843
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                                                                      CA836130.1 GI:26563895
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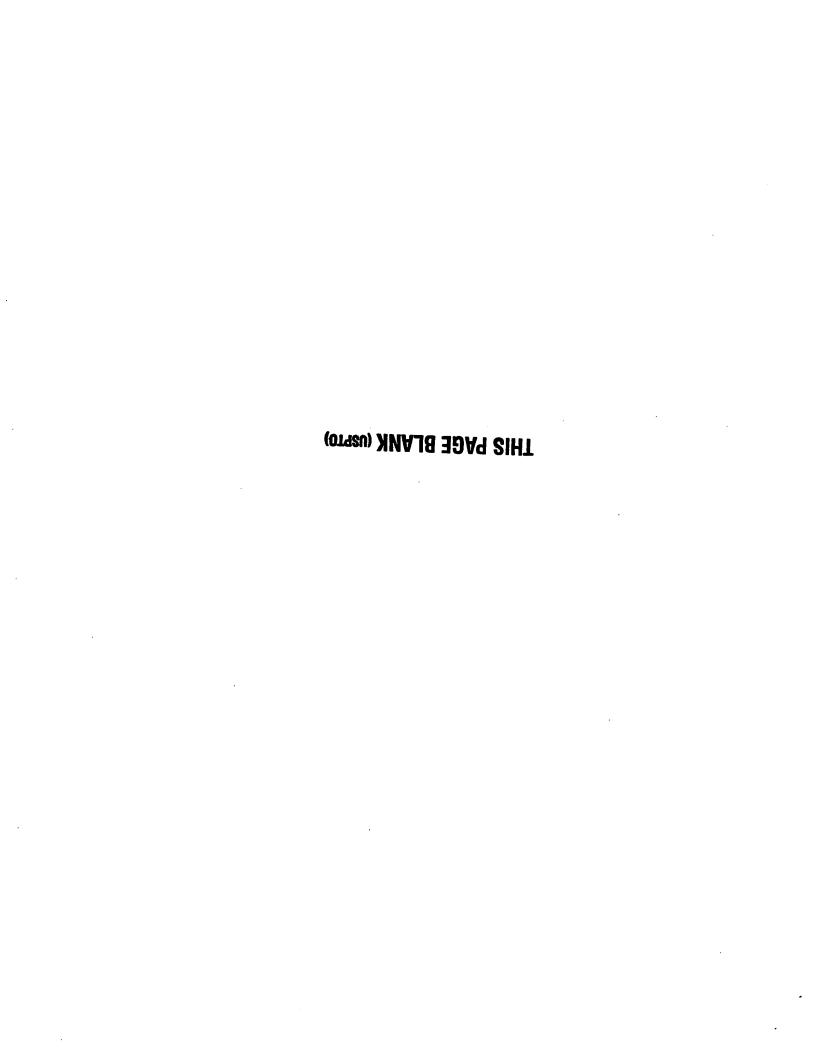
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Job time : 1815 secs

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Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.
Direct Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institude, Bio Resource Center, The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan Phone: 81-298-36-9189, fax: 81-298-36-9199 e-mail: abe@rtc.riken.jp
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Mus musculus molossinus DNA, clone:MSMg01-509123.TJ, genomic survey
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Mus musculus molossinus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
/clone lib="MH"
/note="grown in hydroponics, stress 400 mM NaCl (in 0.5
Hoagland's), 78 h stress"
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BAC end Sequences of Library MSMg01
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/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                               93.8%; Score 15; DB 2; Length 774; 100.0%; Pred. No. 7.7e+02; Live 0; Mismatches 0; Indels
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/mol_type="genomic DNA"
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/clone="MSMg01-509123.TJ"
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AG583208.1 GI:48344038
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                                                                                                               Query Match
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Search completed: May 16, 2005, 06:03:28

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/traislation="MSDNGPQSNQRSAPRITFGGPTDSTDNNQNGGRNGARPKQRRPQ
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KELSPRWYFYLGTGPEASLPYGANKEGIVWATNSCPDDGTGYYRRATRRVRGGDGKM
KELSPRWYFYLGTGPEASLPYGANKEGIVWATPGALTTPKCHIGTRNPNNAATVL
QLPQGTTLPYKGPYAGGSGGSGASRSSRSRGNSRNSTPGSSRGNSPARMAGGGGET
ALALLLLDRLNQLSKVSGKGQQQGGTVTKKSAABASKKRRQKRTATKQYNVTQAFG
RGPBCQTQGRGDQLIRGYGTDYKHWDQIAQPAPSAABSKRRRQKRTATKQYNVTQAFG
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Coronaviridae; Coronavirus.
1 (bases 1 to 1269)
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/note="associated with virus genomic RNA; involved in CTL
                                                                                                                                                                                                                                                                                                                                                             Submitted (26-MAY-2003) Genetic Immunotherapy Lab, Johns Hopkins Singapore, 41 Science Park Road, #03-18 The Gemini, Singapore, Singapore 117610, Singapore Location/Qualifiers

1. 1269
//organism="SARS coronavirus"
               gene, complete cds
AY395001
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AY394985
AY3381174
AY3381174
AY3381175
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Direct Submission
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SARS coronavirus nucleocapsid protein (NP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
/product="nucleocapsid protein"
/protein id="AAP49034.1"
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/db_xref="taxon:227859"
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AY534762S6
AY322205S4
                                      nucleic search, using sw model
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AAALLILDBLNQLESRVSGKGQQQCGTVTKKSAAEASKKPRQKRTATKQYNVTQAFG
RRGPEQTQGNFGDQDL1RQGTDYKHPPQ1AQPAPSASAFFGMSRIGMEVTPSGTWLTY
HGAIKLDDKDPQFKNVVILLAKHIDAYKTFPFTPFPFKKDKKKKTDEAQPLPQRQKKQPT
VTLLPAADMDDFSRQLQNSMSGASADSTQA
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SARs coronavirus HB nucleocapsid protein (NP) gene, complete cds.
AY365036
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KELSPRWYFYYLGTGPEASLPYGANKEGIVWVATEGALNTPKDHIGTRNPNNNAATVL
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SARS coronavirus HPZ-2003

Viruses; seRNA positive-strand viruses, no DNA stage; Nidovirales;

Coronaviridae; Coronavirus

(bases 1 to 1269)

Zhu, H.D., Lu, V.Y., Lu, V.Y., Yao, P.P., Xu, F., Ge, Q., Weng, J.Q.,

Yan, J.Y., Gong, L.M., Shi, W., Zhao, Z.Y. and Zhu, Z.Y.

Cloning and expression of nucleocapsid protein gene of SARS

associated coronavirus
                                                                                                                                                                                                                   AY360146 1269 bp RNA linear VRL 02-SEP-200:
SARS coronavirus HPZ-2003 nucleocapsid protein (NP) gene, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
2 (bases 1 to 1269)
2hu.H.P., Lu.Q.Y., Lu,Y.Y., Yao,P.P., Xu,F., Ge,Q., Weng,J.Q.,
Yan,J.Y., Gong,L.M., Shi,W., Zhao,Z.Y. and Zhu,Z.Y.
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Submitted (04-100)
Submitted (04-100)
Zhejiang Center for Disease Prevention and Control, 17 Lao
Zhi Road, Hangzhou, Zhejiang 310009, P.R. China
Location/Qualifiers
1. .1269
/organism="SARS coronavirus HPZ-2003"
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Pred. No. 7.6;
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/protein_id="AAQ63890.1"
/db_xref="GI:34329619"
                                                                   0; Mismatches
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/db_xref="taxon:243925"
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/gene="NP"
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KELSPRWYFYYLGTGPEASLPYGANKEGIVWVATEGALNTPKOHIGTRNPNNNAATVL
QLPQGTTLPKGFYAEGSRGGSQASSRSSRSRGNSRNSTPGSSRGNSPARMASGGGFT
ALLLLLDBRLNRLESSKVSRGOQOGOTVTKKSAABASKKRRQKRTATKQYNVTQAFG
RRGPEQTQGNFGDODLIRQGTDYKHWPQIAQFAPSASAFFGMSRIGMEVTPSGTWLTY
HGAIKLDBXDPQFRONVILLANKHIDAYKTFPFPFBPKKDKKKKTDEAQPLPQRQKKQPT
VTLLPAADMDDFSRQLQNSMSGASADSTQA"
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SARS coronavirus BJ01 nucleocapsid protein mRNA, complete cds.
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GLPNNTASWFTALTQHGKEELRFPRGQGVPINTNSGPDDQIGYYRRATRRARGGDGKM
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SARS coronavirus HB
SARS coronavirus HB
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
                                                                                                                                         Timani, K.A., Ye.L., Ye,L., Zhu,Y., Wu,Z. and Gong,Z. Cloning, sequencing, expression, and purification of SARS-associated coronavirus nucleocapsid protein for serodiagnosis
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(bases 1 to 1669)

Li,T., Li,X., Chang,Z. and Liu,L.

Identification 6 SARS-COV mRNA leader sequence
Uppublished
                                                                                                                                                                                                                                                J. Clin. Virol. 30 (4), 309-312 (2004)
15163419
2 (bases 1 to 1269)
Timani, K.A., Ye.L., Ye.L., Zhu, Y. and Guo, D.
Direct Submission
Submitted (11-A007-2003) Institute of Virology, Wuhan University,
Wuhan, Hubei 430072, P.R. China
Location/Qualifiers
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Li,T., Li,X., Liu,L. and Chang,Z.
Direct Submission
Submitted (30-JAN-2004) Institute of Biomedicine,Tsinghua
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iive 0; Mismatches 0;
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protein_id="AAR12990.1"

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    organism="SARS coronavirus HB"

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/isolate="HB"
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SARS coronavirus Sin0409
ISM SARS coronavirus Sin0409
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Viruses; SRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
ICE 1 (bases 1 to 1873)
Inm,P.L., Kurup,A., Gopalakrishna,G., Chan,K.P., Wong,C.W.,
Ng,L.C., Se-Thoe,S.Y., Oon,L., Bai,X., Stanton,L.W., Ruan,Y.,
Miller,L.D., Vega,V.B., James,L., Ooi,P.L., Kai,C.S., Olsen,S.J.,
Ang,B. and Leo,Y.S.
Laboratory-acquired severe acute respiratory syndrome (SARS) -
Singapore 2003
                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
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KREBEQTQGRGDQDLIRQSTDVKHWDIAQPAPSASAFRGMSRIGMEVTPSGTWLTY
HGAIKLDDKUPQFKNVILLINKHIDAYKTFPPTEPKKDKKKTDEAQPLPQRQKKQPT
VTPLPAADMDDFSRQLONSMSGASADSTQA"
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Submitted (28-JAN-2004) Genome Institute of Singapore, 60, Biopolis
Street, 02-01, Genome, Singapore 138672, Singapore
Location/Qualifiers
1. 1873
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2 (bases 1 to 1873)
Wei,C.L., Lee,C., Lin,S., Thoreau,H., Vega,V.B., Stanton,L.W. and
                                                                   Submitted (06-JUL-2004) Institute of Biomedicine, Tsinghua University, Beijing, Beijing 100084, China Sequence update by submitter
Sequence update by submitter
( bases 1 to 1669)
Li, T., Li, X., Chang, Z. and Liu, L.
Direct Submission
Submitted (15-SEP-2004) Institute of Biomedicine, Tsinghua University, Beijing 100084, China Sequence update by submitter
On Sep 15, 2004 this sequence version replaced gi:49921010.
Location/Qualifiers
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University, Beijing, Beijing 100084, China 3 (bases I to 1669)
Li,T., Li,X., Liu,L. and Chang,Z.
Direct Submission
                                                                                                                                                                                                                                                                                                     /organism="SARS coronavirus BJ01"
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AX322205S4 2304 bp RNA linear VRL 21-JUL-2003 SARS coronavirus Shanhgai LY Orf7a gene, partial cds; and Orf7b, Orf8b, orf8b, and nucleocapsid protein genes, complete cds. AX322208
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Coronaviridae, Coronavirus.
1 (bases 1 to 1938)
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1 (bases 1 to 2304)
Yuan, Z., Zhang, X., Hu, Y., Lan, S., Wang, H., Zhou, Z. and Wen, Y.
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Laboratory-acquired severe acute respiratory syndrome (SARS) - Singapore 2003
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Wei,C.L., Lee,C., Lin,S., Thoreau,H., Vega,V.B., Stanton,L.W. and
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Pred. No. 7.7;
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SARS coronavirus Sin_WNV
SARS coronavirus Sin_WNV
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KELSPRWYFYYLGTGPEASLPYGANKEGIVWVATEGALNTPKDHIGTRNPNNNAATVL
QLPQCTTLPKGFYAEGSRGGSQASSRSSSRSKGNSRNSTPGSSRGNSPARMASGGGET
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RRGPEGTQGDROFGDQLTRGYTDYKHPDLAQPAPSASAFRGMSRIGMEAAPSGTWLTY
HGAI KLDDKDPQPRQNVILLANKHI DAYKTFPPTEPKKDKKKTDEAQPLPQRQKKQPT
VTLLPAADMDDFSRQLGNSGASADSTQA
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                  Submitted (12-JUN-2003) Molecular Virology, Shanghai Medical
College of Fudan University, 138 Yi Xue Yuan Road, Shanghai 200032,
P.R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="Orf8A"
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2 (bases 1 to 2810)
Wang, Z.G., Li,L.J., Luo,Y., Zhang,J.Y., Wang,M.Y., Cheng,S.Y.,
Zhang,Y.J., Wang,X.M., Lu,Y.Y., Wu,N.P., Mei,L.L. and Wang,Z.X.
Molecular biological analysis of genotyping and phylogeny of severe
acute respiratory syndrome associated coronavirus
Chin. Med. J. 117 (1), 42-48 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (NG-DEC-2003) Department of Microbiology, Zhejiang Center of Disease Prevention and Control, 17 Laozheda Rd., Hangzhou, Zhejiang 310009, China
Nucleotide and amino acid sequences updated by submitter
On Dec 5, 2003 this sequence version replaced gi:31505969.
Location/Qualifiers
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17 Laozheda Rd., Hangzhou,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'translation="MNELTLIDFYLCFLAFLLFLVLIMLIIFWFSLEIQDLEEPCTKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       translation="MFHLVDFQVTIAEILIIIMRTFRIAIWNLDVIISSIVRQLFKPL
/isolation_source="patient with severe acute respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <del>-</del>ω
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="transcription regulatory core sequence
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protein id="AAR27474.1"
db_xref="GI:38735511"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="uncharacterized protein 6"
protein id="AAR27473.1"
db_xref="GI:38735510"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           product="uncharacterized protein 7b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wang, Z., Cheng, S., Zhang, Y., Lu, Y. and Mei, L. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wang, Z., Cheng, S., Zhang, Y., Lu, Y. and Mei, L. Direct Submission
Submitted (03-MA-2003) Department of Microbiof Disease Prevention and Control, 17 Laozhed Zhejiang 310009, China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. 2810
/coganism="SARS coronavirus 2J01"
/mol type="genomic RNA"
/isolate="ZJ01b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="Xiaohong genotype locus 6"
                                                                                                                                                                                                      and its characterization
Chin. Med. J. 116 (9), 1288-1292 (2003)
22889812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:230471"
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SSLTSLLKTHRMCKYTQSTALQELLIQQWIQPMSRRRLLACLCKHKKVSTNLCTHSF
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/db_xref="G1:4132,8999"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAS01069.1"
| Da xref="GGI:41352900"
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FIENKLVKDPPNVQIHTIDGSSGVANPAMDPIYDEPTTTTSVPL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYIIKLVFLWLLWPVTLACFVLAAVYRINWVTGGIAIAMACIVGLMWLSYFVASFRLF
ARTRSMWSFNPETNILLINVPLRGTIVTRPLMESELVIGAVIIRGHLRMAGHSLGRCDI
KDLPKEITVATSRTLSYYKLGASQRVGTDSGFAAYNRYRIGNYKLNTDHAGSNDNIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MKIILFLTLIVFTSCELYHYQECVRGTTVILKEPCPSGTYBGNS
PFHPLADNKPALTCTSTHFAFACADGTRHTYQLRARSVSPKLFIRQEEVQQELYSPLF
LIVAALVFLILCFTIKRKTE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MYSFVSEETGTLIVNSVLLFLAFVVFLLVTLALLTALRLCAYCC NIVNVSLVKPTVYVYSRVKNLNSSEGVPDLLV"
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                                          Chim.S.S.C., Tong,Y.K., Hung,B.C., Chiu,R.W. and Lo,Y.M. Chim.S.B.C., Long, P.K., Hung,B.C., Chiu,R.W. and Lo,Y.M. Submitsed (20-007-2003) Chemical Pathology, Chinese University of Hong Kong, Prince of Wales Hospital, 30-32 Ngan Shing Street,
                                                                                                                                                                                                                                    organism="SARS coronavirus CUHK-L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /codon_start=1
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/protein id="AAS01067.1"
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/db_xref="G1:41352902"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAS01070.1"
/db_xref="GI:41352901"
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/product="orf10"
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                                                                                                                                                                                                                                                                                /mol_type="genomic RNA"
/db_xref="taxon:260550"
                                                                                                                                                            Shatin, Hong Kong, China
Location/Qualifiers
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/product="orf3"</pre>
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/codon_start=1
/product="orf9"
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/codon_start=1
/product="orf8"
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/product="orf7"
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                                                                                                                                                                                                           1. .3080
                                                                                                                                                                                                                                                            /virion
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  Clin. Chem.
                        14709660
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                        PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
JOURNAL
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                                                                                                                                                                                                      /product="uncharacterized protein 8b"
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/db_xref="G1:38735514"
/translation="WGLKILVRYNTRGNTYSTAWICALGKVLPFHRWHTMVQTCTPNV
TINCQDPAGGALIARCWYLHEGHQTAAFRDVLVVLNKRTN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KELSPRWYFYYLGTGPEASLEYGANKEGIYWWATEGALMTPKOHIGTENPUNNAATUL
OLPOGTTLPKGFYAEGSRGSQASSRSSRSRGNSRNSTPGSSRGNSPARMASGGGT
ALLLLLLDRINQLESKYGGKGOQOGOTYTKKSAABASKKPROKRTATKQYNVTQAFG
RRGPEQTGGNFGDDLIRQGTDYKHWPOLAQPAPSASAFFGMSRIGMEVTPSGTWLTY
HGAIKLDKOPOFKNVILLINGHIDAYKTFPPTEPKKDKKKKTDEAQPLPQRQKKQPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'tränslation="MDPNQTNVVPPALHLVDPQIQLTITRMEDAMGGGONSADPKVYP
IILRLGSQLSLSMARRNLDSLEARAFQSTPIVVQMTKLATTEELPDEFVVVTAK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="MLPPCYNFLKEQHCQKASTQREAEAAVKPLLAPHHVVAVIQEIQ
LLAAVGEIILLEWLAEVVKLPSRYCC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /trānslation="MSDNGPQSNQRSAPRITFGGPTDSTDNNQNGGRNGARPKQRRPQ
GLPNNTASWFTALTQHGKEELRFPRGQGVPINTNSGPDDQIGYYRRATRRVRGGDGKM
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1 (bases 1 to 3080)

Chim,S.S.C., Tongy,Y.K., Hung,E.C.W., Chiu,R.W.K. and Lo,Y.M.D.
Genomic Sequencing of a SARS Coronavirus Isolate That Predated the Metropole Hotel Case Cluster in Hong Kong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cds; small
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3080 bp RNA linear VRL 02-FEB-2 SARS coronavirus CUHK-L2 orf4 and orf3 genes, partial cds; small envelope E protein, membrane glycoprotein M, orf7, orf8, orf9, orf10, and orf11 genes, complete cds; nucleocapsid protein gene, barting and orf13 gene, complete cds.
                   product="uncharacterized protein 8a"
fprotein id="AR27476.1"
db xref="G138735513"
f_ranslation="MKLLIVLTCISLCSCICTVVQRCASNKPHVLEDPCKVQH"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/product="uncharacterized protein 9b"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'product="uncharacterized protein 9c"
                                                                                                                                   'note="Xiaohong genotype locus 7"
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                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/product="nucleocapsid protein"
/protein id="AAP44772.1"
/db_xref="GI:31505970"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAP69660.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAP69659.1"
/db_xref="GI:31747858"
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SARS coronavirus CUHK-L2
SARS coronavirus CUHK-L2
                                                                                                                                                            952. .1206
codon_start=1
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AY443095.1 GI:41352885
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Best Local Similarity
Matches 21, Conserv
                                                                                                             misc_feature
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VERSION
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TITLE
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VRL 05-NOV-2003
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                                                                                                                                                                                                                                                                                                                                                                                        SARS coronavirus SZ13
SARS coronavirus SZ13
Viruses; SRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
1 (bases 1 to 8581)
Guan, Y., Zheng, B.J., He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L.,
Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L.,
Chan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and
Poon, L.L.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (26-MAY-2003) Microbiology, The University of Hong Kong, University Pathology Building, Queen Mary Hospital, Pokfulam Road, Hong Kong, China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   no DNA stage; Nidovirales;
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SARS coronavirus GZ60
Viruses; sRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus:
1 (bases 1 to 11006)
Guan, Y., Zheng, B.J., He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L.,
Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L.,
Chan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and
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                             Gaps
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                             Indels
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/mol type="genomic RNA"
/isoTate="SZ13"
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Pred. No. 7.7;
; Mismatches 0;
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                             Mismatches
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/country="Hong Kong"
  Pred. No.
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                                                                                                               7072 ACCAGAATGGAGGACGCAATG 7092
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Guan, Y. and Zheng, B.J.
100.08;
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Best Local Similarity 100.
Matches 21; Conservative
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AUTHORS
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REFERENCE
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                                                                                                         /protein_id="AAS01073.1"
| Ab xref="G1:41352904"
| train.lation="MOLKILVRYINGGNIYSTAWLCALGKVLPFHRWHTMVQTCTPNV
TINCQDPAGGALIARCWYLHEGHQTAAFRDVLVVLNKRTN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MDPNOTNVVPPALHLVDPQIQLTITRMEDAMGQGONSADPKVYP
IIIRLGSQLSLSMARRNLDSLEARAFQSTPIVVQMTKLATTEELPDEFVVVTAK"
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1 (bases 1 to 8439)
Guan, Y., Zheng, B.J., He, Y.O., Liu, X.L., Zhuang, Z.X., Cheung, C.L., Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L., Chan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and Poon, L.L.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 8439)
2 (bases 1 to 8439)
2 and Zheng, B.J.
Direct Submission
Submitted (27-MAY-2003) Microbiology, The University of Hong Kong,
University Pathology Building, Queen Mary Hospital, Pokfulam Road,
Hong Kong, China
Location/Qualifiers
  translation="MKLLIVLTCISLCSCIRTVVQRCASNKPHVLEDPCKVQH"
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/mol_type="genomic RNA"
/isolate="SZ1"
/db_xref="taxon:231516"
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protein_id="AAS01074.1"
'db_xref="G1:41352905"
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SARS coronavirus SZ1, partial genome.
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/db_xref="GI:41352906"
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'product="orf13"
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product="orf11"
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/codon_start=1
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SARS coronavirus SZ1
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TITLE
JOURNAL
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AUTHORS
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FEATURES

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Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Connaviridae; Coronavirus.

1 (Dases 1 to 11010)
Guan, Y., Zheng, B.J., He, Y.O., Liu, X.L., Zhuang, Z.X., Cheung, C.L., Chuo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L., Chan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and Poon, L.L.M.
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SARS coronavirus GZ43
Viruses; sRNA positive-strand viruses, no DNA stage; Nidovirales;
Viruses; sRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.

1 (bases 1 to 13471)
Guan, Y., Zheng, B.J., He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L.,
Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L.,
Chan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and
Poon, L.L.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (27-MAY-2003) Microbiology, The University of Hong Kong, University Pathology Building, Queen Mary Hospital, Pokfulam Road, Hong Kong, China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 13471)
Guan, Y. and Zheng, B.J.
Direct Submission
Submitted (27-MAY-2003) Microbiology, The University of Hong Kong,
University Pathology Building, Queen Mary Hospital, Pokfulam Road,
Hong Kong, China
                                                                                                                                                                                                                                                                                                                                                                                Isolation and characterization of viruses related to the SARS coronavirus from animals in southern China Science 302 (5643), 276-278 (2003)
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      SARS coronavirus HKU-66078, partial genome.
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/mol_type="genomic RNA"
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1. .13471
                                                                                                                      SARS coronavirus HKU-66078
SARS coronavirus HKU-66078
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                                                               AY304494.1 GI:34482145
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Guan, Y. and Zheng, B.J.
Direct Submission
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Best Local Similarity
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   DEFINITION
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                     2 (bases 1 to 11006)
Guan, Y. and Zheng, B.J.
Direct Submission
Submitted (27-MAY-2003) Microbiology, The University of Hong Kong,
University Pathology Building, Queen Mary Hospital, Pokfulam Road,
Hong Kong, China
Location/Qualifiers
1. 11006
| Corganism="SARS coronavirus GZ60" |
| Corganism="SARS coronavirus GZ60" |
| Apple="genomic RNA" |
| isolate="GZ60" |
| isolate="GZ60" |
| ibolate="GZ60" |
| ibolate="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronavirus.

(Cononaviruales; Coronavirus.

(Bases 1 to 11010)

Guan, Y., Zheng, B.J., He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L., Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L., Chan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and Poon, L.L.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (27-MAY-2003) Microbiology, The University of Hong Kong,
University Pathology Building, Queen Mary Hospital, Pokfulam Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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/organism="SARS coronavirus HKU-65806"
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SARS coronavirus HKU-65806, partial genome.
AY304493
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/isolate="HKU-65806"
/db_xref="taxon:231520"
/country="Hong Kong"
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SARS coronavirus HKU-65806
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Guan, Y. and Zheng, B.J.
Direct Submission
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Matches 21; Conservative 0
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RESULT 13 AY304493

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100.0%; Score 21; DB 14; Length 13471;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps
/isolate="GZ43"
/db_xref="taxon:231517"
/country="Hong Kong"
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Search completed: May 16, 2005, 02:00:25 Job time : 503.031 secs

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May 15, 2005, 17:17:00 ; Search time 269.391 Seconds (without alignments) 461.466 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
                                                                    OM nucleic - nucleic search, using sw model
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
Result No.	Score	% Query Match	% Query Match Length DB	DB	ID	Description
	1 21	100.0	29751	12	ADJ39000	Adi39000 SARS coro
••	2 17.8	84.8	4457	4	ABL06791	Abl06791 Drosophil
υ	3 17.8	84.8	9051	4	ABL06790	
υ	4 16.8	80.0	1250	7	AAQ50571	Aaq50571 Asparagin
υ	5 16.8	80.0	1453	0	AAQ50573	-
υ	5 16.8	80.0	1640	7	AAQ50575	
U	7 16.8	80.0	1910	7	AAQ50579	
_	8 16.8	80.0	10419	е	AAA55188	
	9 16.8	80.0	27082	4	AAK70447	. Aak70447 Human imm
ਜ	0 16.8	80.0	42432	m	AAA55187	Aaa55187 Cenarchae
0	16.8	80.0	179651	10	ADL13813	Adl13813 Osteoarth
0	2 16.4	78.1	646	4	AAH83969	Aah83969 Papio ham
C 1	3 16.4	78.1	646	4	AAH83967	Aah83967 Papio ham
r C	4 16.4	78.1	63411	12	ADQ97081	Adq97081 Mouse can
r U	5 16.2	77.1	192	4	AAC62139	Aac62139 Murine be
ř	6 16.2	77.1	448	4	ABA58687	Aba58687 Human foe
Ŧ	7 16.2	77.1	448	4	AAI38366	Aai38366 Probe #70
គ	16.2	77.1	448	4	AAK32540	Aak32540 Human bon
Ä	9 16.2	77.1	448	4	AAK06821	Aak06821 Human bra
Ñ	0 16.2	77.1	448	4	ABS32250	Abs32250 Human liv

RESULT 1 RESULT
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Legistics C virus (HCV); (4) inducing targeted RNA interference toward HCV in hepatic cells; (5) inhibiting replication of HCV; (6) a vector comprising a DNA segment encoding the RNA molecule; (7) a host cells carrying the vector of (6); (8) inhibiting replication of HCV in cells carrying HCV; (9) treating hepatitis C in a subject; (10) a modified carrying HCV; (9) treating hepatitis C in a subject; (10) a modified signal adouble-stranded RNA molecule of 10-30 uncleotides in length, which mediates RNA interference toward a target agent or virus and is linked to at least one receptor-binding ligand; and collections have antiinflammatory, hepatoropic and virucide activities.

(11) inducing targeted RNA interference in a patient. The modified siRNA cells are useful for inactivating virus in mammalian cells. The siRNAs are useful for treating hepatitis C virus, hepatitis B virus, hepatitis D virus, hepatitis E virus, Ebola virus, influence virus, networkus, poliovirus, human papilloma virus, recovirus, poliovirus, human papilloma virus, metapneumoniavirus or coronavirus infections. The methods of the invention can be used to correct or compensate for cellular physiological aborantities involved in conferring susceptibility to viral infections in patients.

The present sequence represents the SARS coronavirus nucleotide sequence,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and
stranded RNA molecule of 10-30 nucleotides that inhibits replication of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell
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Pred. No. 3.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.
              insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL16175) and the encoded proteins (ABB57737-ABB72072). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                          Gaps
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cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster expressed polynucleotide SEQ ID NO 14852.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         developmental biology; cell signalling; insecticide;
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                                                                                                                                     Seguence 4457 BP; 1222 A; 1176 C; 1212 G; 847 T; 0 U; 0 Other;
                                                                                                                                                                      Score 17.8; DB 4; Length 4457;
Pred. No. 1.2e+02;
0; Mismatches 2; Indels 0
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90.5%; Pred. No. 1.-
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11-JUL-2000; 2000US-00614150.
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Best Local Similarity 90.5
Matches 19; Conservative
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                                                                                                                                                                                                            19; Conservative
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A gene encoding asparaginylendopeptidase is claimed. 8 DNA sequences are given (AAOSO559-66). The enzyme is a procease derived from a seed of Canavalia ensiformis which selectively hydrolyses C-terminus amide bond of L-asparagine residue (see AAR4303 and AAR43041). The enzyme is useful for protein fragmentation and enzymatic peptide synthesis. The primers given in AAOSO576-77 and AAOSO583-90 were used in the isolation of the fragments given in AAOSO569-75 and AAOSO569-75 and AAOSO569-75 and AAOSO578-79, by PCR. (Updated on 25-WAR-2003 to correct PA field.)
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                  Asparaginylendopeptidase; Canavalia ensiformis; seed; L-asparagine;
primer; PCR; protein fragmentation; peptide synthesis; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 22-24; 35pp; Japanese.
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                                                                                                       Location/Qualifiers
3. .1094
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Best Local Similarity 90.0%;
Matches 18; Conservative
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(first entry)
                                                                       Canavalia ensiformis.
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P-PSDB; AAR43038.
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24-MAY-1994
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                                                                                                         Key
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Pred. No. 3.1e+02;
0; Mismatches 2; Indels 0
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                                                                                                                      AAQ50571 standard; cDNA to mRNA; 1250 BP
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                    2942 ACCAGAATGGAGGAGGCAGTG 2922
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1. .957
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1 ACCAGAATGGAGGACGCAATG 21
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Best Local Similarity 90.0°
Matches 18; Conservative
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P-PSDB; AAR43036.
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24-MAY-1994
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24-MAY-1994
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                                      gene for encoding asparaginyl endo-peptidase - comprises 8 specified
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                                                                                                                                                                                                                           Sequence 1640 BP; 533 A; 288 C; 383 G; 436 T; 0 U; 0 Other;
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229. .1551
                                                                              Disclosure; Page 26; 35pp; Japanese
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P-PSDB; AAR43040.
             WPI; 1993-373587/47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cenarchaeum symbiosum open reading frame nucleotide sequence SEQ ID NO:3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acids and proteins isolated from the non-thermophilic crenarchaeote Cenarchaeum symbiosum, useful in characterizing the physiology of these archae and in therapeutic, industrial or laboratory
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                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cenarchaeum symbiosum; non-thermophilic; crenarchaeote; physiology; characterisation; archae; therapeutic; industrial; laboratory; ds.
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                                                                                                   Length 1910;
                                                 Sequence 1910 BP; 591 A; 339 C; 464 G; 516 T; 0 U; 0 Other;
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Pred. No. 4e+02;
0; Mismatches 2;
                                                                                                80.0%; Score 16.8; DB 2;
90.0%; Pred. No. 3.2e+02;
ive 0; Mismatches 2;
(Updated on 25-MAR-2003 to correct PA field.)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schleper C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9044 ccadadredacdarecaare 9063
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                                                                                                                                                             Conservative
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nes 18; Conserv
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2000US-0233065P.
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2000US-0234234P.
2000US-0234938P.
2000US-0235484P.
2000US-0235484P.
2000US-0235334P.
2000US-02353484P.
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2000US-0240960P.
2000US-0241221P.
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2000US-0246476P.
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2000US-0246474P.
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2000US-0241787P
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2000US-0249213P.
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2000US-0256719P
 14-SEP-2000; 14-SEP-2000; 28-SEP-2000; 21-SEP-2000; 21-SEP-2000; 22-SEP-2000; 22-SE
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05-DEC-2000;
05-DEC-2000;
05-DEC-2000;
  Human, immune, haematopoietic, immune/haematopoietic antigen, cancer;
cytostatic, gene therapy, vaccine, metastasis, ds.
                                                                    Human immune/haematopoietic antigen genomic sequence SEQ ID NO:25259
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2000US-0184664P.
2000US-0189834P.
2000US-0190076P.
2000US-019123P.
2000US-0205515P.
2000US-020515P.
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2000US-0225270P.
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                                        06-NOV-2001 (first entry)
                                                                                                                                                                  WO200157182-A2
                                                                                                                                         Homo sapiens
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-SEP-2000;
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              AAK70447;
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Determining susceptibility of an individual to joint space narrowing, osteophyte development and/or joint pain comprises identifying whether the individual has at least one polymorphism in a polymucleotide encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a method of determining susceptibility of an individual to joint space narrowing and/or osteophyre development and/or joint pain comprising identifying whether the individual has at least one polymorphism in a polymucleotide encoding at least one of the protein
                                                                                                                                                                                                                            proteins isolated from the non-thermophilic crenarchaeote Cenarchaeum symbiosum. The nucleic acids and proteins identified in the present invention are useful in characterising the physiology of these archae and can be used in therapeutic, industrial or laboratory techniques. AAA55227
                                                                                                                                                                                                          AAA55186 to AAA55226 and AAY90913 to AAY90951 represent nucleic acids and
                                                                                                   crenarchaeote Cenarchaeum symbiosum, useful in characterizing the physiology of these archae and in therapeutic, industrial or laboratory
                                                                                                                                                                                                                                                                                              to AAA55260 represent promoter sequences from Cenarchaeum symbiosum. AAA55261 to AAA55269 represent PCR primers and probes used in examples
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ds; gene; osteopathic; antiinflammatory; antiarthritic; gene therapy; joint space narrowing; osteophyte development; joint pain; osteoarthritis; SNP; single nucleotide polymorphism.
                                                                                                                                                                                                                                                                                                                                                                      Sequence 42432 BP; 8792 A; 12248 C; 12606 G; 8786 T; 0 U; 0 Other;
                                                                                    nucleic acids and proteins isolated from the non-thermophilic
                                                                                                                                                                                                                                                                                                                                                                                                      80.0%; Score 16.8; DB 3; Length 42432; 90.0%; Pred. No. 4.8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 345; 297pp; English.
              Schleper C;
                                                                                                                                                                         Claim 1; Page 75-87; 210pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9046 ccadacredaedarecaare 9065
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                                                                                                                                                                                                                                                                                                                                     from the present invention
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              Swanson RV, Feldman RA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-559141/52.
                                                 WPI; 2000-293148/25
                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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                                                                                                                                        cechniques
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ADL13813/c
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                                                                                                                                                                                                                                                                                                                                              AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (1)
amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic
activity, and can be used in gene therapy and vaccine production. (1)
proteins and polynucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (1) expression. For
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (1) by expressing inactive proteins or to
supplement the patients own production of (1). Additionally, (1)
cuplement displays be used to produce the secreted (1), by inserting the
nucleic acids into a host cell and culturing the cell to express the
protein. (1) proteins and polynucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-related diseases, especially
cancers and cancer metastases of haematopoietic derived cells. AAK64703
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54912 to AAK54950 and AAM82169
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                                                                                                                                                                                                                                                             Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 27082 BP; 5963 A; 7786 C; 7711 G; 5622 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 25259; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cenarchaeum symbiosum nucleotide sequence variant B SEQ ID NO:2.
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              2000US-0251856P.
2000US-0251868P.
2000US-0251869P.
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2000US-0251990P.
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                                                                                                                     05-JAN-2001; 2001US-0259678P
                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DIVE-) DIVERSA CORP
                                                                                                                                                                                                                              WPI; 2001-483426/52.
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Best Local Similarity
Matches 18; Conserv
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                                                                  08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
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                                                                                                                                                                                             Ковеп СА,
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               useful for modulating the susceptibility of an individual to joint space associated with a disease, preferably osteoathritis. The cell line and the non-human animal are useful for screening for an agent for diagnosing an individual having susceptibility to joint space narrowing and/or sosteophyte development and/or joint pain. This sequence corresponds to the polynucleotide encoding a protein listed in the specification. (Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to olfactory receptors (AAG98412-AAG98609) and the genes encoding them (AAH83879-AAH84131) including pseudogenes of 10 primate species, mouse and human. The nucleic acids and receptors may be used in the food processing industry (e.g. for the detection of aromas, quality control and sample analysis), in perfumery (e.g. for the analysis or comparison of perfumes) and in the environment (e.g. for the detection of toxic substances and/or trapping of odours)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding primate and murine olfactory receptors, useful for analysis odors e.g. in food processing and perfumery.
                                                                                                                                                                                                                           Sequence 179651 BP; 48335 A; 39400 C; 42185 G; 49731 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Olfactory receptor; primate; mouse; human; food processing industry; aromas; perfumery; toxic substance; ds.
   composition and agent are
                                                                                                                                                                                                                                                               80.0%; Score 16.8; DB 10; Length 179651; 90.0%; Pred. No. 5.7e+02; rive 0; Mismatches 2; Indels 0; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 646 BP; 136 A; 167 C; 122 G; 221 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Papio hamadryas olfactory receptor pseudogene 3.
 listed in the specification. The methods,
                                                                                                                                                                                       ftp.wipo.int/pub/published_pct_sequences)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 195-196; 482pp; English
                                                                                                                                                                                                                                                                                                                                                                                 157352 CAAGAATGGAGGAAGCAATG 157333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH83969 standard; DNA; 646 BP
                                                                                                                                                                                                                                                                                                                                             2 CCAGAATGGAGGACGCAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-DEC-1999; 99US-0171746P.
21-DEC-2000; 2000US-00747155.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rouquier S, Giorgi D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-381911/40.
                                                                                                                                                                                                                                                                                 Local Similarity
les 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Papio hamadryas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH83969;
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                                                                                                                                                                                                                                                                                                       Matches
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88666666666688888
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The invention relates to olfactory receptors (AAG98432-AAG98609) and the genes encoding them (AAH83879-AAH84131) including pseudogenes of 10 primate species, mouse and human. The nucleic acids and receptors may be used in the food processing industry (e.g. for the detection of aromas, quality control and sample analysis), in perfumery (e.g. for the analysis or comparison of perfumes) and in the environment (e.g. for the detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding primate and murine olfactory receptors, useful for analysis odors e.g. in food processing and perfumery.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                     Olfactory receptor; primate; mouse; human; food processing industry; aromas; perfumery; toxic substance; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Mouse; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78.1%; Score 16.4; DB 4; Length 646; 94.4%; Pred. No. 4.4e+02; ive 0; Mismatches 1; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 646 BP; 135 A; 166 C; 123 G; 222 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer associated sequence MD10-004, SEQ ID 57.
                                                                                                                                                                          Papio hamadryas olfactory receptor encoding gene 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or comparison of perfumes) and in the environm of toxic substances and/or trapping of odours)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 193; 482pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADQ97081 standard; DNA; 63411 BP
478 CAGAATGGAGGAGGCAAT 461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 478 CAGAATGGAGGAGGCAAT 461
                                                                                     AAH83967 standard; DNA; 646 BP.
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21-DEC-2000; 2000US-00747155.
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                                                                                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Giorgi D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-381911/40.
P-PSDB; AAG98485.
                                                                                                                                                                                                                                                Papio hamadryas.
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                                                                                                                                              25-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-OCT-2004
                                                                                                                                                                                                                                                                                                          28-JUN-2001
                                                                                                                 AAH83967;
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                                                        AAH83967/c
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Best Local Similarity 94.4 Matches 17; Conservative

Query Match Matches

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Gaps

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78.1%; Score 16.4; DB 4; Length 646; 94.4%; Pred. No. 4.4e+02; tive 0; Mismatches 1; Indels (

us-10-808-187a-2474.rng

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Search completed: May 16, 2005, 01:09:31
                                                                                                                                                                                                                                                           1 ACCAGAATGGAGGACGCAATG 21
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Best Local Similarity 85.7
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                               Job time : 274.391 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New C2GnT-M polypeptides having core 2, core 4 and I branching beta-1-6-N -acetylglucosaminyltransferase activities for preparing reagents useful for diagnosing, preventing or treating inflammation or tumor metastasis.
                                                                                                                                                                                                  New isolated cancer associated nucleic acids comprising at least 10 contiguous nucleotides, useful for diagnosing, preventing and/or treating cancers such as leukemia and lymphoma.
                                                                                                                                                                                                                                                                                   The present invention relates to cancer associated sequences (ADQ97025-ADQ98004). The sequences are useful for the diagnosis, prevention and/or treatment of cancer, such as leukemia and lymphoma. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formate directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; beta-1-6-N-acetylglucosaminyltransferase; C2GnT-M; inflammation; membrane protein; branched sialyl Lex; L-selectin; immune reaction; inflammation; tissue rejection; tumour metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 63411 BP; 17408 A; 15472 C; 14344 G; 15847 T; 0 U; 340 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 78.1%; Score 16.4; DB 12; Length 63411; Best Local Similarity 94.4%; Pred. No. 7.9e+02; Matches 17; Conservative 0; Mismatches 1; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Murine beta-1-6-N-acetylglucosaminyltransferase DNA fragment.
                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 57; 199pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18892 AGAATGGAGGAGGCAATG 18875
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                                                        22-DEC-2003; 2003WO-US041389
                                                                                   27-DEC-2002; 2002US-00330773
                                                                                                              SAGR-) SAGRES DISCOVERY INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 AGAATGGAGGACGCAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC62139 standard; DNA; 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-MAR-2001 (first entry)
                                                                                                                                           Morris DW, Malandro MS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BURN-) BURNHAM INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-040238/05.
                                                                                                                                                                       WPI; 2004-543781/52.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAB30519
WO2004060304-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-JAN-1999;
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                          22-JUL-2004
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The present sequence encodes a beta-1-6-N-acetylglucosaminyltransferase fragment. The full length polypeptide has core2, core4 and I branching activities. It is designated C26AT-M. C26AT-M is a membrane protein that is predominantly expressed in colon, small intestine, trachea, stomach and thyroid, as well as in certain cancer cell lines. C2GAT-M singlypeptides may be used to prepare molecules having highly branched sialyl Lex and Leslectins, which may be subsequently used to modulate immune reactions, e.g. inflammation and tissue rejection, and to prevent or inhibit tumour metastasis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 192 BP; 48 A; 48 C; 51 G; 45 T; 0 U; 0 Other;
Example 5; Col 33-34; 25pp; English.
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Accaccardeagracecaare 39

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Gaps

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Score 16.2; DB 4; Length 192; Pred. No. 4.8e+02; 0; Mismatches 3; Indels (

77.1%; 85.7%;

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May 16, 2005, 00:11:05; Search time 78.5859 Seconds (without alignments) 437.251 Million cell updates/sec
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*

(cgn2_6/ptodata/1/ina/5B_COMB.seq:*

(cgn2_6/ptodata/1/ina/6A_COMB.seq:*

(cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*

(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

(cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                       1202784 seqs, 818138359 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                     OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                        1 accagaatggaggacgcaatg
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21
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 3, Appli Sequence 1531, A Sequence 1531, A Sequence 9, Appli Sequence 1972, Ap Sequence 1786, A Sequence 278, App 21, Appl 17, Appl 54, Appl 54, Appl 54, Appl 54, Appl Description Sequence 1 Sequence 1 Sequence 2 Sequence Descriptions Sequence US-09-408-020-3 US-09-408-020-2 US-09-409-016-15231 US-09-233-506-9 US-09-949-016-17486 US-09-949-016-17486 US-09-949-016-17486 US-09-949-016-17486 US-09-289-18-278 US-09-289-18-278 US-09-429-755-278 US-09-429-755-278 US-09-949-016-81705 US-09-949-016-81705 US-09-949-016-174507 US-09-949-016-17507 US-09-949-016-17507 SUMMARIES Query Match Length DB 1248 56976 101674 10419 42432 75799 126237 152331 125192 126237 Score Result No. υυυ טטט υυυ

Sequence 3746, Ap Sequence 19028, A Sequence 15, Appl Sequence 11, Appli Sequence 3346, Ap Sequence 27937, A Sequence 128820, Sequence 1159, Ap Sequence 1159, Ap Sequence 20, Appl Sequence 20, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 5, Appli	CENARCHAEUM SYMBIOSUM	Length 10419; Indels 0; Gaps	CENARCHAEUM SYMBIOSUM
4 US-09-270-767-19028 4 US-09-936-145-15 4 US-09-996-137-1 4 US-09-99-016-14184 US-09-248-796A-3362 4 US-09-248-796A-3362 4 US-09-949-016-27937 4 US-09-949-016-27937 4 US-09-949-016-27937 4 US-09-949-016-27937 4 US-09-949-016-27937 3 US-08-753-247-13 3 US-08-753-247-13 3 US-08-753-247-8 1 US-08-753-247-8 1 US-08-773-254A-5 2 US-08-773-254A-5	ALIGNMENTS on US/09408020 Rohald V. Robert A. Christa NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM P.002A NUMBER: US/09/408,020 1999-09-29 1999-09-29 1123 r Windows Version 3.0 um symbiosum	.0%; Score 16.8; DB 4; .0%; Pred. No. 1e+02; e 0; Mismatches 2; GCAATG 21 GCAATG 9063	1 US/09408020 nnald V. cobert A. Christa TCLEIC ACIDS AND PROTEINS FROM 002A MBER: US/09/408,020 1999-09-29 188: 60/102,294 188-09-29 1133
C 28 15.4 73.3 669 C 29 15.4 73.3 669 C 33 15.4 73.3 1581 C 32 15.4 73.3 18310 C 32 15.4 73.3 18310 C 32 15.2 72.4 574 C 36 15.2 72.4 601 C 36 15.2 72.4 1002 C 37 15.2 72.4 1002 C 40 15.2 72.4 1758 C 41 15.2 72.4 1758 C 42 15.2 72.4 1758 C 43 15.2 72.4 1758 C 44 15.2 72.4 2130 C 45 15.2 72.4 1758 C 47 15.2 72.4 1758 C 48 15.2 72.4 2130 C 48 15.2 72.4 2130	RESULT 1 US-09-408-020-3 Sequence 3, Application US/09408020 Patent No. 663291 GENERAL INFORMATION: APPLICANT: Schleper, Christa TITLE OF INVENTION: NUCLEIC ACIDS AN FILE REFERENCE: DCORP.002A CURRENT APPLICANT: 1999-09-29 FILE REFERENCE: DCORP.002A CURRENT FILING DATE: 1999-09-29 PRIOR FILING DATE: 1999-09-29 NUMBER OF SEQ ID NOS: 123 SOFTWARE: FastSEQ for Windows Versic SEQ ID NO 3 TYPE: DNA ORGANISM: Cenarchaeum symbiosum FEATURE: AMME/KEY: CDS LOCATION: (1)(10419) US-09-408-020-3	Query Match Best Local Similarity 90.0%; Matches 18; Conservative Qy 2 CCAGAATGGAGGAGGAAT Db 9044 CCAGAGTGGAGGATGCAAT	RESULT 2 US-09-408-020-2 Sequence 2, Application US/09408020 Patent No. 6632937 GENERAL INFORMATION: APPLICANT: Swanson, Robert A. APPLICANT: Schleper, Christa TITLE OF INVENTION: NUCLEIC ACIDS A! FILE REFERENCE: DCORP.002A CURRENT FILING DATE: 1999-09-29 PRIOR APPLICATION NUMBER: G0/102,29 PRIOR APPLICATION NUMBER: 60/102,29 PRIOR APPLICATION NUMBER: 60/102,29 PRIOR FILING DATE: 1998-09-29 NUMBER OF SEQ ID NOS: 123 SOFTWARE: FastSEQ for Windows Versi

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Query Match
Best Local Similarity 85.7;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: (1)..(192)
US-09-233-506-9
     ; OKGANISM: MUMBANISM: MANAGENISMI
ORGANISM: Human
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US-09-233-506-9/c
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Sequence 15231, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLOOD.307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 15231

LENGTH: 75799
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 CCAGAATGGAGGACGCAATG 21
                                                   ORGANISM: Cenarchaeum symbiosum
                                                                                                                                                                                                                                                                                                  CDS (23558)...(24862)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
(34559)...(36067)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: CDS
; LOCATION: (39454)...(40572)
US-09-408-020-2
                                                                                                                                       NAME/KEY: CDS
LOCATION: (10625)...(11434)
                                                                                                                                                                                          NAME/KEY: CDS
LOCATION: (11478)...(13046)
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(13046)...(14620)
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LOCATION: (37002)...(37403)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: CDS
LOCATION: (37404)...(38282)
                                                                     FEATURE:
NAME/KEY: CDS
LOCATION: (3)...(10421)
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US-09-949-016-15231/c
                LENGTH: 42432
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NAME/KEY:
LOCATION:
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LOCATION:
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LOCATION:
                                    TYPE: DNA
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                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                FEATURE:
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                                                                                                                        FEATURE
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Sequence 1972, Application US/09489039A

Sequence 1972, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:
APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUMBER: OS 109,20489,039A

TITLE REFERENCE: 2709,2004001

CURRENT APPLICATION NUMBER: US/09/489,039A

CURRENT BILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117,747

PRIOR APPLICATION NUMBER: US 60/117,747

SEQ ID NO 1972

SEQ ID NO 1972
                                                                                                                                                                                                                                                              Sequence 9, Application US/09233506;
Sequence 9, Application US/09233506;
Patent No. 6136580
GENERAL INPORMATION:
APPLICANT: Fukuda, Minoru
TITLE OF INVENTION: Core 2, Core 4 and I Branches
TITLE OF INVENTION: Core 2, Core 4 and I Branches
TITLE OF INVENTION: US/09/233,506
CURRENT APPLICATION NUMBER: US/09/233,506
CURRENT FILING DATE: 1999-01-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 9
LENGTH: 192
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Query Match

80.0%; Score 16.8; DB 4; Length 75799;
Best Local Similarity 90.0%; Pred. No. 1.4e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1248;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.1%; Score 16.2; DB 3; Length 1:
85.7%; Pred. No. 1.1e+02;
tive 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
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                                                                                                                                                             43216 CCAGAATGAAGGACACAATG 43197
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; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-1972
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13868 ACCAGTATGGAGGAGGAATG 13888
                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Seattle
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US-09-062-451-278
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                                                                          Fraction NO. Gelidials associated by Prince Renewation:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CLOO1307

CURRENT FILING DATE: 2000-04-14

FRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 17486

LENGTH: 56976
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GENERAL INCORNATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-0-09-88
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRAESEQ for Windows Version 4.0
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77.1%; Score 16.2; DB 4; Length 101674;
Best Local Similarity 85.7%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0;
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                                      Sequence 17486, Application US/09949016 Patent No. 6812339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; NAME/KEY: misc_feature; LCATION: (1)...(56976); CTHER INFORMATION: n = A,T,C or G US-09-949-016-17486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 85.77
Matches 18, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Human
                 JS-09-949-016-17486
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ORGANISM: Human
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LENGTH: 101674
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1 ACCAGAATGGAGGACGCAATG 21

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Gaps
                                                                                          APPLICANT: Frudakis, Tony N.
Smith, John M.
Reed, Steven G.
TITLE OF INVENTION: CROSSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF BREAST CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
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Patent No. 6344550
GENERAL INFORMATION:
APPLICANT: Smith, John M.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
TILLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER NUMBER OF SEQUENCES: 297
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75.2%; Score 15.8; DB 3;
89.5%; Pred. No. 2e+02;
tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Potter, Jane E. R.
REGISTRATION UNDRER: 33,332
REFERENCE/DOCKET NUMBER: 210121.419C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed IP Law Group
STREET: 701 Fifth Avenue, Suite 6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,789A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQUENCE DESCRIPTION: SEQUENCE DESCRIPTION: SEQ ID NO: 278:
US-08-991-789A-278
; Sequence 278, Application US/08991789A
; Patent No. 6225054
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 11-Dec-1997
CLASSIFICATION: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (206) 682-60:
INFORMATION FOR SEQ ID NO: 278:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 292
                                                                                                                                                                                                                                                                                                                                      STATE: Washington
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Best Local Similarity 89.5°
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Indels
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       0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (1)...(452)
; OTHER INFORMATION: n = A,T,C or G
US-09-429-755-278
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LOCATION: (1).T.(452)
OTHER INFORMATION: n = A,T,C or G
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                                                                                             109 CCAGAATGGAGGCTGCAAT 127
                                                 2 CCAGAATGGAGGACGCAAT 20
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Best Local Similarity 89.5%;
Matches 17; Conservative (
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Reed, Steven G.
Smith, John M.
Misher, Linda E.
Dillon, Davin C.
Retter, Marc W.
                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Frudakis, Tony N.
APPLICANT: Smith, John M.
APPLICANT: Reed, Steven G.
       17; Conservative
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ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapien
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APPLICANT:
APPLICANT:
       Matches
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APPLICANT: Frudakis, Tony N.
APPLICANT: Shith, John M.
APPLICANT: Shith, John M.
APPLICANT: Misher, Lynda
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: COMPOSITION OF SHEAST CANCER
FILE REFERENCE: 210121.419C5
CURRENT APPLICATION NUMBER: US 09/062,451
EARLIER APPLICATION NUMBER: US 08/991,789
EARLIER FILING DATE: 1999-04-17
EARLIER FILING DATE: 1997-10-11
EARLIER FILING DATE: 1997-01-10
EARLIER FILING DATE: 1997-01-10
EARLIER FILING DATE: 1997-01-10
EARLIER FILING DATE: 1997-01-10
EARLIER FILING DATE: 1996-08-20
EARLIER FILING DATE: 1996-01-01
EARLIER FILING DATE: 1996-01-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 75.2%; Score 15.8; DB 3; Length 452; Best Local Similarity 89.5%; Pred. No. 2e+02; Matches 17; Conservative 0; Mismatches 2; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPILICATION NUMBER: US/09/062,451
FILING DATE: 04-APR-1997
CLASSIFICATION:
                                                                                                                                                                                                 ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.419C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 682-4900
TELEPHONE: (206) 682-6931
INFORMATION FOR SEQ ID NO: 278:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 base pairs
TYPE: nucleic acid
STRANDENNESS: Single
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 278
LENGTH: 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 278, Application US/09289198
Patent No. 6586570
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OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity
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Gaps
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APPLICANT: Reiter, Marc W.
APPLICANT: Reiter, Marc W.
APPLICANT: Reiter, Marc W.
APPLICANT: Builon, Davin C.
TITLE OF INVENTION: TREATMENT AND DIAGNOSIS OF BREAST CANCER; FILE REFERENCE: 210121.419C6
CURRENT APPLICATION NUMBER: US/09/429,755A
CURRENT FILING DATE: 1999-10-28
NUMBER OF SEQ ID NOS: 315
SEQ ID NO 278

"TOTAL OF TREATMENT OF TREATMENT AND SEQ ID NOS: 315
"SEQ ID NO 278
"TOTAL OF TREATMENT OF 
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APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF BREAST CANCER FILE REFERENCE: 210121.419610
CURRENT APPLICATION NUMBER: US/09/699,295
CURRENT FILING DATE: 2000-10-26
NUMBER OF SEQ ID NOS: 326
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 278
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Pred. No. 2e+02;
0; Mismatches 2; Indels
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; ORGANISM: Human
US-09-949-016-81707
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
TITLE OF INVENTION: WIMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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Bacter No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REPERENCE: CL001307
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                                      Query Match 75.2%; Score 15.8; DB 4; Length 452; Best Local Similarity 89.5%; Pred. No. 2e+02; Matches 17; Conservative 0; Mismatches 2; Indels (
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Pred. No. 2.1e+02;
0; Mismatches 2; Indels 0
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CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PRESSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                         Sequence 81705, Application US/09949016 Patent No. 6812339
                                                                                                                                                        109 CCAGAATGGAGGCTGCAAT 127
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89.5%;
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Best Local Similarity 89.55
Matches 17; Conservative
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; ORGANISM: Human
US-09-949-016-81706
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LENGTH: 601
US-09-699-295-278
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LENGTH: 601
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Qy 1 ACCAGANGGACA 19

Qy 1 ACCAGANGGACA 151

Bb 169 ACCAGANGGACA 151

Bb 169 ACCAGANGGACAA 151

Bc 36-0-16-81707/c

; Sequence 81707, Application US/09949016
; Patent No. 681239
; GRNERAL INFORMATEN, PLOTAMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLO01307
; CURRENT FILING DATE: 2000-40-14
; PRIOR PELING DATE: 2000-40-16
; CURRENT FILING DATE: 2000-40-16
; PRIOR PELING DATE: 2000-10-03
; PRIOR PELING DATE: 2000-10-03
; RING PELING DATE: 2000-10-03
; SOFTWARES FERSES (6/231,498
; PRIOR PELING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARES FERSES (6/231,498
; RING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARES FERSES (6/231,498
; RING DATOT
; LEWGTH: 601
; TYPE: DNA
; TYPE: D
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May 16, 2005, 02:00:36 ; Search time 995.531 Seconds (without alignments) 129.102 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT NEW PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 2474, Sequence 16, Ap Sequence 4 Sequence 7 Sequence 1 Sequence 3 Description Sequence Sequence. Sequence Sequence US-10-808-187-2474 US-10-699-936-16 US-10-699-936-11 US-10-899-936-11 US-10-889-447-5 US-10-889-447-6 US-10-889-447-6 US-10-889-447-7 US-10-889-447-7 US-10-889-447-7 US-10-889-447-7 US-10-889-747-7 US-10-889-747-7 US-10-889-747-7 SUMMARIES П Query Match Length DB 29430 29727 29727 2304 2304 24774 28920 28920 29291 1000.0 1000.0 1000.0 1000.0 1000.0 Score

Result No.

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ALIGNMENTS

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APPLICANT: Taylor, Jill
APPLICANT: Scholl, David B.
APPLICANT: Scholl, David B.
APPLICANT: Scholl, David B.
APPLICANT: Wentworth, David B.
APPLICANT: Gomeoficions and Methods for Detecting Severe Acute Respiratory TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory TITLE OF INVENTION: Syndrome Coronavirus
FILE REPERENCE: DHI-07986
CURRENT PILITE OF INVENTION NUMBER: US/10/699,936
CURRENT FILING DATE: 2003-11-03
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.2
SEQ ID NO 11
FIRE TERMINE OF THE TERMINE OF
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US-10-889-447-3

Sequence 3, Application US/10889447

Publication No. US20050075307A1

GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: MODILATION OF AMINOPEPTIDASE N EXPRESSION
FILE REFERENCE: RTS-0685US
CURRENT APPLICATION NUMBER: US/10/889,447

CURRENT FILING DATE: 2004-07-12

PRIOR APPLICATION NUMBER: 60/486,670

PRIOR FILING DATE: 2003-07-12

NUMBER OF SEQ ID NOS: 241

SEQ ID NO 3

SEQ ID NO 3

LENGTH: 24774
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Pred. No. 2.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA; CORGANISM: SARS coronavirus Shanhgai LY
US-10-699-936-11
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Matches 21; Conservative 0
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Best Local Similarity 100.0%;
Matches 21; Conservative 0
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APPLICANT: Gillin-Ross, Laura
APPLICANT: Taylor, Jill
APPLICANT: Scholl, David R.
APPLICANT: Wentworth, David E.
APPLICANT: Wentworth, Joseph D.
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
TITLE OF INVENTION: Syndrome Coronavirus
FILE REFERENCE: DHI-07986
CURRENT APPLICATION NUMBER: US/10/699,936
CURRENT FILING DATE: 2003-11-03
NUMBER OF SEQ ID NOS: 87
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APPLICANT: Taylor, Jaila.
APPLICANT: Scholl, David R.
APPLICANT: Wentworth, David E.
APPLICANT: Joilack, Joseph D.
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
TITLE OF INVENTION: Syndrome Coronavirus
FILE REFERENCE: DHI-07986
CURRENT APPLICATION NUMBER: US/10/699,936
CURRENT APPLICATION NUMBER: US/10/699,936
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.2
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                                                                                                                                                                                                                              OTHER INFORMATION: Description of Artificial Sequence: Primer
                                                                                                                                                                                                                                                                                                                      Score 21; DB 19; Length 21;
Pred. No. 3.3;
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100.0%; Score 21; DB
Best Local Similarity 100.0%; Pred. No. 3.3
Matches 21; Conservative 0; Mismatches
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Publication No. US20050095582A1
GENERAL INFORMATION:
APPLICANT: Gillim-Ross, Laura
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ACCAGAATGGAGGACGCAATG 21
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; ORGANISM: SARS-COV Shanghai LY
US-10-699-936-7
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SEQ ID NO 7
LENGTH: 2304
                                                                                                                                TYPE: DNA ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS: 2476
SOFTWARE: Patentin ver. 3.2
SEQ ID NO 2474
LENGTH: 21
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US-10-699-936-16
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US-10-699-936-7
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Length 29291;
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                                                                                    APPLICANT: Jain, Ravi
TITIE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
FILE REFERENCE: RTS-060LOATION OF AMINOPEPTIDASE N EXPRESSION
CURRENT APPLICATION NUMBER: US/10/889,447
CURRENT FILING DATE: 2004-07-12
PRIOR PRILING DATE: 2003-07-12
NUMBER OF SEQ ID NOS: 241
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TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
FILE REFERENCE: RTS-0685US
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TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 100.0%; Score 21; DB 19; Local Similarity 100.0%; Pred. No. 2.6; les 21; Conservative 0; Mismatches 0;
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100.0%; Pred. No. 2.6;
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CURRENT FILING DATE: 2004-07-12
PRIOR PELLING DATE: 2003-07-12
NUMBER OF SEQ ID NOS: 241
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 29430
                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: SARS coronavirus isolate BJ02
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: n is any nucleotide US-10-889-447-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; LOCATION:
; OTHER INFORMATION: n is any nucleotide
US-10-889-447-7
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    Sequence 4, Application US/10889447
Publication No. US20050075307A1
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/10889447
Publication No. US20050075307A1
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
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Best Local Similarity
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LENGTH: 29291
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; Publication No. US20050075307A1
; GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
; APPLICANT: Jain, Ravi
; TITLE OF INVENTION: MODULATION OF AMINOFEPTIDASE N EXPRESSION
FILE REFERENCE: RTS-0685U8
; CURRENT FILING DATE: 2004-07-12
; PRIOR PILING DATE: 2004-07-12
; PRIOR FILING DATE: 2003-07-12
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 2.6;
                                                                                                                                                                       APPLICANT: Main, Ravi
APPLICANT: Jain, Ravi
TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
FILE REFERENCE: RTS-0685US
CURRENT APPLICATION NUMBER: US/10/889,447
CURRENT FILING DATE: 2004-07-12
PRIOR PAPLICATION NUMBER: 60/486,670
PRIOR FILING DATE: 2003-07-12
NUMBER OF SEQ ID NOS: 241
SOFTWARE: FASTSEQ for Windows Version 4.0
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Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches
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US-10-889-447-5
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23315 ACCAGAATGGAGGACGCAATG 23335
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Sequence 5, Application US/10889447
Publication No. US20050075307A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%;
Matches 21; Conservative 0
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LENGTH: 28920
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LENGTH: 28920
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US-10-889-447-4
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APPLICANT: Taylor, Jill
APPLICANT: Scholl, David R.
APPLICANT: Scholl, David R.
APPLICANT: Scholl, David E.
APPLICANT: Wentworth, David E.
APPLICANT: Wentworth, David E.
APPLICANT: Jollick, Joseph D.
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory;
TITLE OF INVENTION: Syndrome Coronavirus
FILE REFERENCE: DHI-07986
CURRENT APPLICATION NUMBER: US/10/699,936
CURRENT FILING DATE: 2003-11-03
NUMBER OF SEQ ID NOS: 87
SOFTWARE: Patentin version 3.2
SEQ ID NO:
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                                         100.0%; Score 21; DB 19; Length 29727; 100.0%; Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17, Application US/10839729
; Publication No. US20050002953A1
; GENERAL INFORMATION:
; APPLICANT: JOHN HEROIG
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
; TITLE OF INVENTION: AND METHODS OF USE
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: BIODRANK. 013A
; CURRENT FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/468703
; PRIOR APLICATION NUMBER: 60/468703
; RICH FILING DATE: 2003-05-06
; SOFTWARE: FESTESEQ for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 29736
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100.0%; Pred. No. 2.6;
iive 0; Mismatches 0;
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                                                                                                                                                                  28202 ACCAGAATGGAGGACGCAATG 28222
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                                                                                                                                       1 ACCAGAATGGAGGACGCAATG 21
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Best Local Similarity 100.0
Matches 21; Conservative
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US-10-839-729-17
                                                            Best Local Similarity 100.
Matches 21; Conservative
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US-10-889-447-8
                                                                                                                                                                                                                                                         RESULT 13
US-10-699-936-1
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                                           Query Match
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Sequence 1, Application US/1082757

Publication No. US20050004071A1

AERERAL INFORMATION:
APPLICANT: Comper, Wayne

TITLE OF INVENTION: Charged Polysaccharides Resistant To Lysosomal Degradation During

TITLE OF INVENTION: Prevent Infection And Renal Passage And Their Use To Treat Or

TITLE OF INVENTION: Prevent Infection By Coronaviruses

FILE REFERENCE: 112.13-007-999

CURRENT APPLICATION NUMBER: US/10/827,757

CURRENT PILING DATE: 2004-04-20

PRIOR FILING DATE: 2003-04-21
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Publication No. US20050075307A1

GENERAL INFORMATION:

APPLICANT: Bennett, C. Frank

APPLICANT: Jain, Ravi

TILE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION

FILE REFERENCE: RTS-0655US

CURRENT APPLICATION NUMBER: US/10/889,447

CURRENT FILING DATE: 2004-07-12

PRIOR PILING DATE: 2003-07-12

NUMBER OF SEQ ID NOS: 241

SEQ ID NO 8

SEQ ID NO 8

LENGTH: 29727
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100.0%; Score 21; DB 18; Length 29727;
Best Local Similarity 100.0%; Pred. No. 2.6;
Matches 21; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 21; DB 18; Length 29727; Best Local Similarity 100.0%; Pred. No. 2.6; Matches 21; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: SARS-related coronavirus (Urbani strain)
                     FILE REFERENCE: BIOBANK.013A
CURRENT APPLICATION NUMBER: US/10/839,729
CURRENT FILING DATE: 2004-05-04
PRIOR APPLICATION NUMBER: 60/468703
PRIOR FILING DATE: 2003-05-06
                                                                                                                                       NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 29727
TITLE OF INVENTION: AND METHODS OF USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28202 ACCAGAATGGAGGACGCAATG 28222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 1
SOFTWARE: Patentin version 3.2
SEQ ID NO 1
LENGTH: 29727
                                                                                                                                                                                                                                    ; TYPE: DNA; ORGANISM: SARS Coronavirus
US-10-839-729-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
US-10-889-447-8
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US-10-827-757-1
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Sequence 9, Application US/10889447

Sequence 9, Application US/10889447

Sequence 9, Application Wo. US20050075307A1

SEQUENCE 9, Application Wo. US20050075307A1

SEQUENCE 1 No. US20050075307A1

SEQUENCE 1 No. US20050075307A1

SEQUENCE 1 No. USANATION WOMBER: US/10/889,447

CURRENT FILING DATE: 2004-07-12

SURIGN FULING DATE: 2003-07-12

NUMBER OF SEQ ID NOS: 241

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 9

LENGTH: 29736

TYPE: DNA

OURTH: 29736

Query Match

Gaps 0; Indels 0; Indels 0; Gaps 0;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Search completed: May 16, 2005, 14:33:49 Job time : 997.531 secs

28187 ACCAGAATGGAGGACGCAATG 28207

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1 ACCAGAATGGAGGACGCAATG 21

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mRNA linear EST 11-DEC-2003
Xenopus laevis cDNA clone
5', mRNA sequence.
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RZPDI. IMAGP9998RX131.

RZPDLIB; I.M.A.G.E. cDNA Clone Collection (amp- resistant) (RZPDLIB No.998) http://www.rzpd.de/cgi-bin/products/showlib.pl.cgi/response7libNo=998 RZPDLIB; Xenopus Din/products/showlib.pl.cgi/response7libNo=998 RZPDLIB; Xenopus Din/products/showlib.pl.cgi/response7libNo=998 Contact: Ina Rolfs RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101

Fax: +49 30 32639 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="mRNA"
/db_xref="teaxon:8355"
/clone="IMAGp998RC28712; IMAGE:3580537"
/tissue type="haad, stage 30"
/lab host="DH10B (phage-resistant)"
/clone lib="Wellcome CRC pRN3 head"
/note="Vector: pBSRN3; Site_1: Not1; Site_2: EcoRI; cDNAs were oligo-dT primed and directionally cloned. Staging according to Nieuwkoop and Faber. Library was constructed
                                                                                  GR ED06M
GR Ea09E
Drosophil
                                                                                                                                                      CM1-HT114
EST789358
                                                                                                                           OA ABA001
USDA-FP_1
                                                          SWOVEBCAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This clone is available royalty-free from RZPD; contact RZPD (clone@rzpd.de) for further information. Seg primer: RN f, 5' GCAGAAGCTCAGAATAAACGCTC 3'.
                                             Xenopus 1
                                                                        BX678509
                                                                                                                                                                                                               QGC16M16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Xenopodinae; Xenopus; Xenopus.

1 (bases 1 to 470)

Heil,O., Neubert,P., Peters,M., Radelof,U., Schneider,D.,
Schroth,A., Korn,B. and Landgrebe,J.

Xenopus laevis UniGene Set 1 (RZPDLIB No.988)

Unpublished (2003)

Contact: Ina Rolfs

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH

In Neuenheimer Feld 580, D-69120 Heidelberg, Germany
CF342092 / BX858453 / CD362585 / BC043892 /
                                                      AI130642
BX678509
CO124099
CO089699
                                                                                                              AL106874 1
CL91674 (CL916764 (CO64323) 1
BC986407 (CO024225 AQ211924 AQ211944 BBS553927 (BBS60827 (BBS911490 (CO02425) BBS911490 (CO02425) BBS911490 (CO02425) BBS911490 (CO02425) BBS911490 (CO02425) BBS911490 (CO02425)
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Xenopus laevis
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/organism≃"Xenopus laevis"
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BX849505 Wellcome CRC pRN3 head
IMAGp998K028732 ; IMAGE:3580537
                                                      AT1130642
BX678509
CO089699
CNS016KW
CL916764
CO624225
BG986407
CO024225
BG553927
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BX842817
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 764
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321
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509
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RESULT 1
BX849505/c
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KEYWORDS
SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
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JOURNAL
COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
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  BX849505 BX849505
BJ058057 BJ058057
BG160575 df35f01.y
F15026 SSO4H12 Por
BG893390 dae20b11.
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GH12045.5
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                                                                                            ; Search time 2371.69 Seconds
  (without alignments)
  337.038 Million cell updates/sec
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BI446008
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AI110115 CAI134552 CAI134552 CAI134552 CAI
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AI259251
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             5.1.6
Compugen Ltd.
                                                                                                                                                                                                                                                     34239544 seqs, 19032134700 residues
                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                GenCore version
Copyright (c) 1993 - 2005
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first 45 summaries
                                                                   nucleic search, using sw model
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length: 2000000000
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gb_htc.:.;

gb_est4:.;

gb_est5:.;

gb_est6:.;

gb_gss1:.;

gb_gss2:.;
                                                                                            May 16, 2005,
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Maximum
Listing
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Match
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117.8 117.8 117.8 117.8 117.8 117.8 117.8 117.8 117.8 117.8

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Result

Minimum DB seq Maximum DB seq

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Perfect score:

Title:

Sequence:

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Run

Scoring table:

Searched:

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/lab_host="heluoB (plage-resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available through the I.M.A.G.B. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40RP from Gibco
High quality sequence stops: 508.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P15026 286 bp mRNA linear EST 09-SEP-1996 SSO4H12 Porcine small intestine cDNA library Sus scrofa cDNA clone
                            Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 667)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L.,
Person,D., Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y.,
Person,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
Waterston,R. and Wilson,R.
                                                                                                                                                                                                      Mushy Kanopus EST project, 1999
Unpublished (1999)
Contact: Sandy Clifton, Ph.D.
Washy Kanopus EST project, 1999
Washy Kanopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
Fax: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: A.K. Winteroe
Department of Animal Science and Animal Health, Division of Animal
Genetics, The Royal Veterinary and Agricultural University
Bulowsvej 13, 1870 Frederiksberg C, Denmark.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 286)
Wintero, A.K., Fredholm, M. and Davies, W.

Evaluation and characterization of a porcine small intestine cDNA library: analysis of 839 clones
Mamm. Genome 7 (7), 509-517 (1996)
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.4%; Score 19.4; DB 4;
ilarity 95.2%; Pred. No. 1.1e+02;
Conservative 0; Mismatches 1;
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F15026
F15026.1 GI:972497
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nes 20; Conser
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MEDLINE
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Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Xenopus
1 (bases 1 to 566)
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dev stage="stage 25"
/clone_lib="NIBB Mochii normalized Xenopus tailbud
library"
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                                                                                                                         Length 470;
                                                                                                                                                                                         Indels
   by N. Garrett, K. Ryan and A.M. Zorn,
Institute). "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Expressed genes in X. laevis embryo Unpublished (2001)
Contact: Tadaeu Shin-i Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856
                                                                                                                         92.4%; Score 19.4; DB 5; I
larity 95.2%; Pred. No. 1.1e+02;
Conservative 0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL058c18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: tshini@genes.nig.ac.jp
The information of this clone
URL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://xenopus.nibb.ac.jp.
Location/Qualifiers
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BG160575.1 GI:12694494
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 407).
Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
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407 bp mRNA linear EST 05-NOV-200 B0992E02-5 NIA Mouse Unfertilized Egg cDNA Library (Long 1) Mus musculus cDNA clone NIA:B0992E02 IMAGE:30481105 5', mRNA sequence.
                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                    Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 406)
Osada, S., Xitayama, A., Ueno, N. and Taira, M.
Expression analysis of genes which are expressed in the anterior neuroectoderm of Xenopus embryos
   library Xenopus laevis cDNA clone XL427d08ex 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Masanori, Taira
Department of Biological Sciences
Graduate School of Science, University of Tokyo; CREST, Japan Science and Technology Corporation, Japan 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan Tel: 81.03-5841-4434
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National Institute on Aging/National Institutes of Health
National Institute on Aging/National Institutes of Health
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: m taira@biol.s.u-tokyo.ac.jp,
URL:http://www.shigen.nig.ac.jp/nbrp/xenopus/est/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="XL427d08ex"
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                                                                                                                                         Xenopus laevis (African clawed frog)
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                                            BP677561
BP677561.1 GI:46025516
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/mol_type="mRNA"
/db_zref="laxon:8155"
/db_aref="laxon:8155"
/dov_stage="adult"
/dev_stage="adult"
/dev_stage="adult"
/lab_host="bD10B (phage-resistant)"
/clone=lib="NICHD_XGC_Lul"
/clone=lib="NICHD_XGC_Lul"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2.6 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection
(XGC) library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.

Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.

Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing Dy: Washington University Genome Sequencing Center

Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov

High quality sequence stop: 344.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BG893390 367 bp mRNA linear EST 04-JUN-200
dae20b11.x1 NICHD_XGC_Lu1 Xenopus laevis cDNA clone IMAGE:4674405
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopodinae; Xenopus; Xenopus.
1 (bases 1 to 367)
NCI-CBASP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                         Gaps
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/clone lib="Porcine small intestine cDNA library"
/note="directionally cloned cDNA in XL1-blue MRF'"
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                                                                                                                                                                                                                                                                 Score 17.8; DB 7;
Pred. No. 6.2e+02;
0; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                272 ACCAGAATGGGGGATGCAATG 252
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ilarity 90.5%;
Conservative
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Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3', mRNA sequence.
BG893390
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Best Local Similarity
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Best Local Similarity
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ORGANISM
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BG893390/c
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TITLE
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90.5%;
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90.5%;
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Unpublished (1997)
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Matches 19; Conservative
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: pCMV-SPORT6 (Invitrogen); Site_1: Sall;
Site_2: Not1; Mouse cDNA project by the Laboratory of
Genefics, National Institute on Aging (NIA), Intramural
Research Program, NIH (http://lgsun.grc.nia.nih.gov/cDNA).
This is a long-transcript enriched cDNA library (Ref
Genome Ress. 11: 1553-1558 (2001). [PMID: 11544199]). Total
RNAs were extracted from a pool of 1488 unfertilized eggs.
Double-stranded cDNAs were synthesized with an Oligo(dT)
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                                                                                                                           /clone="NIA:B0992E02 IWAGE:30481105"
/dev stage="Unfertilized Egg"
/lab_host="DH10B"
/clone_lib="NIA Mouse Unfertilized Egg cDNA Library (Long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Email: http://www.fruitfly.org/EST,
Plate: EK.2142 row: E column: 7
High quality sequence stop: 432.
Location/Qualifiers
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterrygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Kopczynski, C., Platt, D., Campbell, J., Muzong, C., Laufer, A.,
Peterson, E. and Swimmer, C.
Exelixis Flyrag EST Project CK01 Library
Unpublished (2004)
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EK214255.5prime Exelixis FlyTag CK01 pCDNA-SK+ Drosophila
melanogaster cDNA clone EK214255 5, mRNA sequence.
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84.8%; Score 17.8; DB 7; Length 407;
Best Local Similarity 90.5%; Pred. No. 6.5e+02;
Matches 19; Conservative 0; Mismatches 2; Indels (
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One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
                                                                                          /db_xref="niaEST:B0992E02-5"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (fruit fly)
                                      organism="Mus musculus"
Location/Qualifiers
                                                       'mol_type="mRNA"
'strain="C57BL/6J"
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CO296590.1 GI:49218273
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COMMENT
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: Kenopus clones from this library are available
through the I.M.A.G.E. Consortium/LINL at: info@image.llnl.gov
High quality sequence stop: 442.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     513 bp mRNA linear EST 21-AUG-2001 dai34h08.y2 NICHD_XGC_Sp1 Xenopus laevis cDNA clone IMAGE:4963815 5', mRNA sequence.
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/clone_"EK214255"
/clone_lib="Exelixis FlyTag CK01 pCDNA-SK+"
/note="Organ: mixed stage embryos, imaginal disks, and
adult heads; Vector: pCDNA-SK+; Site_1: NotI; Site_2:
XhoI; Random primed, normalized library from mixed stage
embryos, imaginal disks, and adult heads."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev stage="adult"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NICHD XGC_Spl"
/clone_lib="NICHD XGC_Spl"
/note="Yogan: spleen; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sall; Cloned unidirectionally. Primer: Öligo dT.
Average insert size 2.4 kb. Constructed by Life
__nerhnologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                  Score 17.8; DB 7; Length 4
Pred. No. 6.5e+02;
0; Mismatches 2; Indels
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Pred. No. 6.6e+02;
0; Mismatches 2;
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Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Xenopus laevis"
/mol_type="mRNA"
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1 (bases 1 to 513)
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/note="Vector: pT7T3-Pac; Site 1: EcoRI; Site 2: NotI; PolyA-selected mRNA was prepared from unfertilized Xenopus laevis eggs. The library was constructed in the vector pT7T3-Pac as described in Bonaldo, M.F., Lennon, G. and Soares, M.B. 'Normalization and subtraction: two approaches to facilitate gene discovery', Genome Research 6:791-806, 1996. The first strand synthesis used a NotI-dT18 primer; double stranded oDNAs were ligated to EcoRI adapters, disested with NotI, and directionally cloned into the NotI and EcoRI-digested pT7T3-Pac vector. The library contained approximately 7.2 X 10^5 recombinants, with average insert sizes of 1-1.5 kb."
                             Staffa, N.G.
                                                                                                                                                                                                                                 Contact: Perry J. Blackshear
Affice of Clinical Research and Laboratory of Signal Transduction
National Institute of Environmental Health Sciences
A2-05 NIEHS, 101 Alexander Drive, Research Triangle Park, NC 27709,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Clone is available through Research Genetics, Inc., 2130 Memorial Parkway, Huntsville, AL 35901 phone 800-533-4363 ext.cdna, fax 256-536-9016 att:cdna, email
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lr.cd2CF_13G04_M13R_Earthworm Cadmium Exposure Library Lumbricus rubellus cDNA clone Lr_Cd2CF_13G04_5', mRNA sequence.
CF610686.1 GI:37191864
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA Sequencing and analyses performed by National Institutes of Health Intramural Sequencing Center (NISC).
                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Blackshear/Soares normalized Xenopus egg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                Blackshear, P.J., Lai, W.S., Thorn, J.M., Kennington, E.A., Staf Jr., Moore, D.T., Bouffard, G.G., Beckstrom-Sternberg, S.M., Towlman, J.W., Bonaldo, M.F. and Soares, M.B.
The NIEMS Kenopus maternal EST project: interim analysis of first 13,879 ESTe from unfertilized eggs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue_type="unfertilized egg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell_type="unfertilized egg"
/dev_stage="unfertilized egg"
/lab_host="DH108"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Xenopus laevis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /mol_type="mRNA"
/db_xref="taxon:8355"
/clone="PBX0089H06"
                                                                                                                                                                                                                                                                                                                                                                                                                Email: black009@niehs.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BACKWARD: CAGGAAACAGCTATGACC
Plate: 0089 row: H column:
Seg primer: T7 primer.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sex="female"
     (bases 1 to 585)
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                                                                                                                                                                                                                                                                                                                                                                 Tel: 919 541-4899
                                                                                                                                                                                                                                                                                                                                                                                               541-4571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /dev state="0-3 day old Ore-R males"
/lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
/lab_host="Plates AT.10-AT.120: DH5-alpha. Plates
/lab_host="1319: DH5-alpha ToonA"
/clone_lib="AT Drosophila melanogaster adult testes pOTB7"
/note="Organ: ADULT testes; Vector: pOTB7; Site 1: ECORI; Site_2: Xho1; The mRNA for the testis library was made from testes and seminal vessicles hand dissected from 0-3 day old Ore-R males. RNA kindly provided by the lab of Margaret Fuller. Sized fractionated cDNAs were directly ligated into pOTB7. Plasmid cDNA library."
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library Xenopus
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                           EST 23-APR-2001
                                                                                                                                                                                                                                               Eukaryota; Merazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Bekaryota; Merazoa; Arthropoda; Brachycera; Muscomorpha; Bphydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 577)
Stapleton,M., Brokstein,P., Hong,L., Agbayani,A., Baxter,E., Berman,B., Carlson,J., Champe,M., Chavez,C., Chew,M., Dorsett,V., Farfan,D., Frise,E., George,R., Gonzalez,M., Guarin,H., Harris,N., Farfan,D., Frise,E., George,R., Gonzalez,M., Guarin,H., Harris,N., Pacleb,J., Paragas,V., Park,S., Mungall,C.J., Nuncoo,J., Pacleb,J., Parks,S., Phouanenavong,S., Wan,K., Yu,C., Lewis,S.E., Celniker,S. and Rubin,G.M.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae;
                     BG635276 ST7 bp mRNA linear EST 23-APR-20
TAT31804.5prime AT Drosophila melanogaster adult testes pOTB7
Drosophila melanogaster cDNA clone AT31804 5 similar to CG3845:
FBan0003845 located on: 2R 49E1-49E1;: 04/10/2001, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
hit genomic AE003820: arm:2R [7816709,8082095]
estimated-cyto:49D1-49F2: 04/10/2001
Plate: AT.318 row: A column: 4
High quality sequence stop: 574.
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90.5%; Pred. No. 6.7e+02;
ive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
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Drosophila melanogaster
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/db_xref="taxon:7227"
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                                                                                                                                                     BG635276.1 GI:13762813
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BG635276
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AI134552 607 bp mRNA linear EST 19-APR-2001 GH12045.5prime GH Drosophila melanogaster head pOT2 Drosophila melanogaster cDNA clone GH12045 5prime, mRNA sequence.
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/dev_stage="adult"
/lab_host="DH5 - alpha"
/clone_lib="GH Drosophila melanogaster head pOT2"
/note="Organ: head, Vector: pOT2; Site_1: EcoR1; Site_2:
Xho1; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."
                                                                                                                                          /dev_stage="adult"
/lab_host="DH5 - alpha"
/clone_lib="GH Drosophila melanogaster head pOT2"
/note="Organ: head, Vector: pOT2; Site_1: EcoR1; Site_2:
XhoI; Sized fractionated cDNAs were directly ligated into
pOT2. Plasmid cDNA library."
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BDGP/HHMI Drosophila EST Project
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 120 row: D column: 9
High quality sequence stop: 514.
Location/Qualifiers
1. 607
/organism="Drosophila melanogaster"
/db xref="type="mRNA"
/db xref="type="mRNA"
/clone="GH12045"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                               Length 601;
                                                                                                                                                                                                                                                                                                                                            Score 17.8; DB 1; Length 6
Pred. No. 6.7e+02;
0; Mismatches 2; Indels
                                           'organism="Drosophila melanogaster"
                                                                                                                                     /sex="male and female"
                                                            /mol_type="mRNA"
/db xref="taxon:7227"
Location/Qualifiers
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                                                                                                          clone="GH09580"
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90.5%;
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Best Local Similarity 90.55
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                    Email: chaseley@cardiff.ac.uk, Kille@cardiff.ac.uk
Sequencing was performed in Cardiff using the pBluescriptII XR cDNA
library (Stratagene) protocol.
            Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
Lumbricina; Lumbricidae; Lumbricus.
1 (bases 1 to 597)
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Lewis,S. and Rubin,G.M.
BDGP/HHMI Drosophila EST Project
                                                                                     Chaseley, J., Hedley, B.A., Morgan, J.C., Sturzenbaum, S., Blaxter, M. and Kille, P.
The Lumbricus rubellus EST program - Sequences from a Cadmium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / mol_type="mRNA"

/mol_type="mRNA"

/do_xref="taxon:35632"

/clone="tx_Cd2CF 13604"

/tissue_type="Whole worm"

/dev stage="Adult"

/clone_lib="Earthworm Cadmium Exposure Library"

/note="Vector: pBluescript II SK+; The library was prepared using protocols given by the supplier

(Stratagene)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lawrence Berkeley National Lab
One Cyclotron Rd, Berkeley, CA 94720, USA
Fax: 510 486 6798
Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
Plate: 95 row: G column: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Drosophila melanogaster
Eukaryota, Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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84.8%; Score 17.8; DB 7; Length 597;

Best Local Similarity 90.5%; Pred. No. 6.7e+02;

Matches 19; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                 BIOSI 1
Cardiff University
Main College, Museum Avenue, Cardiff, CF11 3TL,
Tel: +44 2920876680
Fax: +44 2920874305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BACKWARD: caggaaacagctatgaccatg
Plate: 13 row: G column: 04
Seq primer: caggaaacagctatgaccatg
High quality sequence stop: 440.
Location/Qualifiers
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                                                                                                                                                                                   Unpublished (2003)
Contact: Jennifer Chaseley
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EST.
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  Lumbricus rubellus
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                                                                                                                                                                     Exposure library
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Gaps

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BJ078249 MIBB Mochii normalized Xenopus tailbud library Xenopus lacvis cDNA clone XL063j06 3', mRNA sequence.
BJ078249.1 GI:17523165
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                                                                                                                                                                               Xenopus laevis

Wetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus;

Meses 1 to 607)

Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and
                                                                                                                                                                                                                                                                                                           Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Conter For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp
The information of this clone is available through the following URL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Location/Qualifiers
Location/Qualifiers
lorganism="xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="xLu63j06"
/tissue_type="whole embryo"
/dev_stage="stage 25"
/clone lib="NIBB Mochii normalized Xenopus tailbud
library"
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                                                                                                                                                              Xenopus laevis (African clawed frog)
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Best Local Similarity 90.54
Matches 19; Conservative
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RESULT 15
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Search completed: May 16, 2005, 06:03:36 Job time : 2379.69 secs

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In Unpublished

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E. 3 (bases 1 to 1269)

E. 3 (bases 1 to 1269)

E. 4 (bases 1 to 1269)

E. 5 (bases 1 
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| OLPQCTTLPKGFYAEGSRGGSQASSRSSRRGNSRNSTPGSSRGNSPARMASGGGET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VRL 02-SEP-2003
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SARS coronavirus HPZ-2003
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.

1 (bases 1 to 1269)
Zhu,H.P., Lu,Q.Y., Lu,Y.Y., Yao,P.P., Xu,F., Ge,Q., Weng,J.Q., Yan,J.Y., Gong,L.M., Shi,W., Zhao,Z.Y. and Zhu,Z.Y.
Cloning and expression of nucleocapsid protein gene of SARS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene, complete
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Compugen Ltd.
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              GenCore version
Copyright (c) 1993 - 2005
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ALALLLDRLNRLESRVSGKGQQQCQTVTKKSAAEASKKPRQKRTATKQYNVTQAFG
RKSPEQTQGNFGDQLIRQCTDYKHWPQIAQPAPSASAFFGMSRIGMEVTPSGTWLTY
HGAIKLDDKOPQFKNVILLIKHIDAYKTFPFPTEPKKDKKKKTDEAQPLPQRQKKQPT
VTLLPAADMDDFSRQLQNSMSGASADSTQA"
                                                                                                                                                                                                                                                                                    AY365036 1269 bp RNA linear VRL 01-JUN-2004
SARS coronavirus HB nucleocapsid protein (NP) gene, complete cds.
AY365036
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GLPNNTASWFTALTQHGKEBLRFPRGQGVPINTNSGPDDQIGYYRRATRRARGGDGKM
KELSPRWYFYYLGTGPPEASLPYGANKEGIVWVATEGALNTPKDHIGTRNPNNNAATVL
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ALALILIDRINQLESKVSGKGQQQGGTVTKKSAAEASKKPRQKRTATKQYNVTQAFG
KREPEQTGGROEDQDLIRGGTDYKHWPQLAQFAPSASAFFGMSRIGMEVTPSGTWLTY
HGAIKLDDKOPQFKNVILLINKHIDAYKTFPPTEPKKDKKKTDEAQPLPQRQKKQPT
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1 (bases 1 to 1269)
11 (hases 1 to 1269)
12 (hani, X.A., Ye,L., Ye,L., Zhu,Y., Wu,Z. and Gong,Z. Cloning, sequencing, expression, and purification of SARS-associated coronavirus nucleocapsid protein for serodiagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (11-AUG-2003) Institute of Virology, Wuhan University, Wuhan, Hubei 430072, P.R. China Location/Qualifiers
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Timani, K.A., Ye, L., Ye, L., Zhu, Y. and Guo, D.
Direct Submission
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protein id="AAR12990.1"
/db_xref="G1:38176102"
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/virion
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/country="China: Wuhan, Hubei"
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J. Clin. Virol. 30 (4), 309-312 (2004)
15163419
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                                                                                                                                         0; Mismatches
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/isolate="HB"
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/gene="NP"
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/gene="NP"
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Best Local Similarity 100.0
Matches 25; Conservative
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                                                                                                                                         25; Conservative
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Best Local Similarity
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AY365036/c
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AY322205S4 2304 bp RNA linear VRL 21-JUL-2003 SARS coronavirus Shanhgai LY Orf7a gene, partial cds; and Orf7b, Orf8b, and nucleocapsid protein genes, complete cds.
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GENNUTASKTTALTOHGKEELRF PREGGVPLINTRGADOLGYYRRATRRYRGGDGKN
KELSPRWY FYLGTGPEASLIPYGANKEGI VWVATEGALNTP FUDLI GTRNPINNAATVI
QLPQCTTL PKGFYAGGSGGSGASRS SSRSGNSRNSTRNST PGSSRGNSPARMAGGGGET
ALALLILDRINQLESKVSGRGQQQGGTVTKKSAABASKKRRQKRTATKQYRVTQAFG
KRGPRQTQGRGDQDLIRQCTDY KRWPQLAQPSSABFFGWSRIGMETTY
HGAIKLDDKOPQFKNVILLINKHIDAYKTPPPTEPKKUKKKTDEAQPLPQRKKQPT
VTPLPAADMDDFSRQLQNSMSGASADSTQA"
AYS36760 1669 bp mRNA linear VRL 15-SEP-2004
SARS coronavirus BJ01 nucleocapsid protein mRNA, complete cds.
AYS36760
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Sequence update by submitter
On Sep 15, 2004 this sequence version replaced gi:49921010.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (16-UTL-2004) Institute of Biomedicine, Tsinghua University, Beijing, Beijing 100084, China Sequence update by submitter (bases I to 1669)
Li,T., Li,X., Chang,Z. and Liu,L.
Direct Submission
Submitted (15-SEP-2004) Institute of Biomedicine, Tsinghua
                                                                                                                                                                                                                                                                                                                                                                               Unpublished
2 (bases I to 1669)
Li,T., Liu,L. and Chang,Z.
Li,T., Liu,L. and Chang,Z.
Direct Submission
Submitted (30-JAN-2004) Institute of Biomedicine,Tsinghua
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100.0%; Score 25; DB 14; Length 1
Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                               Viruses; ssRNA positive-strand viruses, no DNA coronaviridae; Coronavirus.

1 (bases 1 to 1669)

Li,T., Li,X., Chang,Z. and Liu,L.
Identification of SARS-CoV mRNA leader sequence Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="SARS coronavirus BJ01"
/mol type="mRNA"
/strain="BJ01"
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/product="nucleocapsid protein"
/protein_id="AAS48456.1"
/db_xref="GI:44889746"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              University, Beijing, Beijing 100084, 3 (bases 1 to 1669)
Li,T., Li,X., Liu,L. and Chang,Z.
Direct Submission
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/country="China"
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                                                                                                         AY536760.3 GI:52100973
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SARS coronavirus BJ01
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KEYWORDS
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uncharacterized protein 8a, uncharacterized protein 8b, nucleocapsid protein, uncharacterized protein 9b, and uncharacterized protein 9c genes, complete cds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Zhejiang 310009, China
4 (bases 1 to 2810)
Wang,Z., Cheng,S., Zhang,Y., Lu,Y. and Mei,L.
Direct Submission
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/product="uncharacterized protein 6"
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/country="China: Hangzhou"
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db_xref="GI:38735511"
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/isolate="ZJ01b"
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1. .2810
                                                                                    AY290752.2 GI:38735509
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SARS coronavirus ZJ01
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4 of 4 SARS coronavirus Shanhgai LY SARS coronavirus Shanhgai LY Viruses; serRA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.

1 (bases I to 2304)

Yann, Z., Zhang, X., Hu, Y., Lan, S., Wang, H., Zhou, Z. and Wen, Y. Direct Submission
Submitted (12-JUN-2003) Molecular Virology, Shanghai Medical College of Fudan University, 138 Yi Xue Yuan Road, Shanghai 200032, P.R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="Orf8b"
/protein id="AAP82973.1"
/db_xref="G1:32454351"
/translation="MULKILVRYNTRGNTYSTAWLCALGKVLPFHRWHTMVQTCTPNV
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                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAP82970.1"
| Dax xref="grd:32454348"
| translation="REPCPSATYEGNSPFHPLADNKFALTCTSTHFAFACADGTRHTY
| QLRARSUSPKLPIRQEEVQQELYSPLFLIVAALVFLILCFTIKRKTE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /trānslation="MSDNGPQSNQRSAPRITFGGPTDSTDNNQNGGRNGARPKQRRPQ
GLPNNTASWFTALTQHGKEELRFPRGQGVPINTNSGPDDQIGYYRRATRRVRGGDGKM
KELSPRWYFYYLGTGPEASLPYGANKEGIVWVATEGALNTPKDHIGTRNPNNNAATVL
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KREBEQTGGRFGDQDLIRQGTDYKHWPQLAQPAPSASAFFGMSRIGMEAAPSGTWLTY
HGALKLDDKQPFNVJLLINKHIDAYKTFPPTEPKKDKKKTDEAQPLPQRQKKQPT
VTLLPAADMDDFSRQLONSMSGASADSTQA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MNELTLIDFYLCFLAFLLFLVLIMLIIFWFSLEIQDLEEPCTKV"
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                                                                                                                                                                                                                                     /wordenism="SARS coronavirus Shanhgai LY"
/mol type="genomic RNA"
/db xrefe="taxon:235173"
/country="China: Shanghai"
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/produce="nucleocapsid protein"
/protein id="AAP82974.1"
/db_xref="GI:32454352"
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Pred. No. 0.033;
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/db_xref="G1:32454349"
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/db_xref="GI:32454350"
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/product="Orf7a"
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/product="Orf7b"
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/product="Orf8A"
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AY290752/c
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Wang, Z.G., Li,L.J., Luo,Y., Zhang,J.Y., Wang,M.Y., Cheng,S.Y., Zhang,Y.G., Li,L.J., Lu,Y.Y., Wu,N.P., Mei,L.L. and Wang,Z.X. Molecular biological analysis of genotyping and phylogeny of severe accute respiratory syndrome associated coronavirus Chin. Med. J. 117 (1), 42-48 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (05-DEC-2003) Department of Microbiology, Zhejiang Center of Disease Prevention and Control, 17 Laozheda Rd., Hangzhou, Zhejiang 310009, China Nucleotide and amino acid sequences updated by submitter On Dec 5, 2003 this sequence version replaced gi:31505969.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zhejiang Center
Hangzhou,
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Viruses; SSRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.

1 (bases 1 to 2810.)

Li,L., Wang,Z., Lu,Y., Bao,Q., Chen,S., Wu,N., Cheng,S., Weng,J., Zhang,Y., Yan,J., Mei,L., Wang,X., Zhu,H., Yu,Y., Zhang,M., Li,M., Yao,J., Lu,Q., Yao,J., Wo,J., Wang,S. and Hu,S. Severe acute respiratory syndrome-associated coronavirus genotype chin. Med. J. 116 (9), 1288-1292 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /isolation_source="patient with severe acute respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               <u>.</u>9
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           Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.

1 (bases 1 to 3080)
Chim,S.S.C., Tong,Y.K., Hung,E.C.W., Chiu,R.W.K. and Lo,Y.M.D.
Genomic Sequencing of a SARS Coronavirus Isolate That Predated the Metropole Hotel Case Cluster in Hong Kong
Clin. Chem. 50 (1), 231-233 (2004)
                                                                                                                                                                                    2 (bases 1 to 3080)
Chim.S.S.C., Tong,Y.K., Hung,E.C., Chiu,R.W. and Lo,Y.M.
Direct Submission
Submitted (20-007-2003) Chemical Pathology, Chinese University
Hong Kong, Prince of Wales Hospital, 30-32 Ngan Shing Street,
                                                                                                                                                                                                                                                                                                                                 1. .3080 /organism="SARS coronavirus CUHK-L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="orf9"
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Location/Qualifiers
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SARS coronavirus CUHK-L2
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KREPEQTQGRFGDQDLIRQCPDVKHWPQLAQFAPSASAFFGMSRIGMEYTPSGTWLTY
HGALKLDDKUPQFKNVTLLINKHIDAYKTFPPTEPKKDKKKTTDEAQPLPQRQKKQPT
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                                                                                                                                                                                                                                                                                                                                                                                             /translation="MCLKILVRYNTRCNTYSTAWLCALGKVLPFHRWHTWVQTCTPNV
TINCQDPAGGALIARCWYLHEGHQTAAFRDVLVVLNKRTN"
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                                         'translation="MNELTLIDFYLCFLAFLLFLVLIMLIIFWFSLEIQDLEEPCTKV
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SARS coronavirus CUHK-L2 orf4 and orf3 genes, partial cds; small envelope E protein, membrane glycoprotein M, orf7, orf8, orf9, orf10, and orf11 genes, complete cds; nucleocapsid protein gene, partial cds; and orf13 gene, complete cds.
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/note="transcription regulatory core sequence 9"
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                                                                                 861. .866
/note="transcription regulatory core sequence
867. .986
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Best Local Similarity 100.0%; Pred. No. 0.033;
Matches 25; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /codon_start=1
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SARS coronavirus CUHK-L2
                                                                                                                                                                                                                                                                                              952. .1206
/codon_start=1
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                                                                                      misc_feature
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AY443086S10/c
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VRL 05-NOV-2003

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Viruses; SSRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.

1 (bases 1 to 8581)

1 ubases 1 to 8581)

1 ubases 1 to 8581, He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L., Chuo, S. W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K. L., Chan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and Poon, L.L.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SARS coronavirus GZ60
SARS coronavirus GZ60
Viruses; seRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
1 (bases 1 to 11006)
Guan, Y., Zheng, B.J., He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (26-MAY-2003) Microbiology, The University of Hong Kong, University Pathology Building, Queen Mary Hospital, Pokfulam Road, Hong Kong, China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolation and characterization of viruses related to the SARS coronavirus from animals in southern China Science 302 (5643), 276-278 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 25; DB 14; Length 8581; llarity 100.0%; Pred. No. 0.033; Conservative 0; Mismatches 0; Indels 0
                                                                                                             14; Length 8439;
                                                                                                                                                                                                                                                                                                                        linear
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/organism="SARS coronavirus SZ13"
                                                                                                               100.0%; Score 25; DB 14
100.0%; Pred. No. 0.033;
                                                                                                                                                                                                                                                                                                                      AY304487
SARS coronavirus SZ13, partial genome.
AY304487
AY304487.1 GI:34482138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SARS coronavirus GZ60, partial genome. AY304491
                                                                                                                                                  0; Mismatches
 /mol_type="genomic RNA"
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                                                                                                                                                                                                           7156 GCTGTGAACCAAGACGCAGTATTAT 7132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTGTGAACCAAGACGCAGTATTAT 7126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol type="genomic RNA"
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                                                                                                                                                                                       1 GCTGTGAACCAAGACGCAGTATTAT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GCTGTGAACCAAGACGCAGTATTAT 25
                                                        /country="Hong Kong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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Guan, Y. and Zheng, B.J.
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SARS coronavirus SZ13
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Best Local Similarity
Matches 25; Conserva
                                                                                                                              Similarity
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Best Local {
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VERSION
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KEYWORDS
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                                                                                                                                                                                                     /protein_id="AaS01073.1"
| Maxace="equ: 41352904"
| translation="WOLKILVRYNTRGNTYSTAWLCALGKVLPFHRWHTMVQTCTPNV
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                                                                                                                                                                                                                                                                                                                                                                         /protein_id="AAS01075.1"
| db_xree===01:41352906"
| translation="MENDOTNUVPALHLVDPQ1QLTITRMEDAMGGGQNSADPKVYP
| ILIRIGSQLSLSMARRNLDSLEARAFOSTP1VVQMTKLATTEELPDEFVVVTAK"
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translation="MNELTLIDFYLCFLAFLLFLVLIMLIIFWFSLEIQDLEEPCTKV
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1 (Dases 1 to 8439)
Guan, Y., Zheng, B.J., He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L., Chuo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L., Chan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and Poon, L.L.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (27-MAY-2003) Microbiology, The University of Hong Kong,
University Pathology Building, Queen Mary Hospital, Pokfulam Road,
                                                                                         _protein_id="AASO1072.1"
'db_xref="GI:41352903"
'translation="MKLLIVLTCISLCSCIRTVVQRCASNKPHVLEDPCKVQH"
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protein_id="AAS01074.1"
db_xref="G1:41352905"
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rtial genome.
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/codon_start=1
/product="orf11"
                                                                      product="orf10"
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                                                        codon_start=1
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Guan, Y. and Zheng, B.J.
Direct Submission
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SARS coronavirus SZ1
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Best Local Similarity
Matches 25; Conserv
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SOURCE
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AY304489/c
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AUTHORS
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1 (bases 1 to 13471)
Guan, Y., Zheng, B.J., He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L., Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L., Ponn, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and
                                                                                                                                                                                                                                                              Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.

1 (bases 1 to 11010)
Guan, Y., Zheng, B.J., He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L., Luo, S.W., Lin, P.H., Zhang, L.J., Guan, X.J., Butt, K.M., Wong, K.L., Chan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and Poon, L.L.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (27-MAY-2003) Microbiology, The University of Hong Kong,
University Pathology Building, Queen Mary Hospital, Pokfulam Road,
Hong Kong, China
                                                                                                                                                                                                                                                                                                                                                                                                                Isolation and characterization of viruses related to the SARS coronavirus from animals in southern China Science 302 (5643), 276-278 (2003)
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                                                                                                                                AY304494 11010 bp RNA
SARS coronavirus HKU-66078, partial genome.
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Pred. No. 0.033;
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AY304490
AY304490.1 GI:34482141
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/isolate="HKU-66078"
/db_xref="taxon:231521"
/country="Hong Kong"
      9561 GCTGTGAACCAAGACGCAGTATTAT 9537
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SARS coronavirus HKU-66078
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100.0%; Pre
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Guan, Y. and Zheng, B.J.
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Guan, Y. and Zheng, B.J.
Direct Submission
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SARS coronavirus GZ43
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Best Local Similarity
Matches 25; Conserv
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                                                                                          RESULT 11
AY304494/c
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LOCUS
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AUTHORS
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MEDLINE
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SOURCE
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Viruses; SRNA positive-strand viruses, no DNA stage; Nidovirales; Coronavirus HTG-5806
Oronavirus positive-strand viruses, no DNA stage; Nidovirales; 1 to 11010)
Guan, Y., Zheng, B.J., He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L., Chan, K.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L., Chan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and Poon, L.L.M. and animals in southern China coronavirus from animals in southern China Science 302 (5643), 276-278 (2003)
                                                                                                                                        1295836

2 (bases 1 to 11006)

Guan, Y. and Zheng, B.J.

Direct. Submission-2003) Microbiology, The University of Hong Kong,

Submitted (27-MAY-2003) Microbiology, The University of Hong Kong,

University Pathology Building, Queen Mary Hospital, Pokfulam Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (27-MAY-2003) Microbiology, The University of Hong Kong, University Pathology Building, Queen Mary Hospital, Pokfulam Road, Hong Kong, China
Luo,S.W., Li,P.H., Zhang,L.J., Guan,Y.J., Butt,K.M., Wong,K.L.,
Chan,K.W., Lim,W., Shortridge,K.F., Yuen,K.Y., Peiris,J.S.M. and
Poon,L.L.M.
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                                                                   Isolation and characterization of viruses related to the SARS coronavirus from animals in southern China Science 302 (5643), 276-278 (2003)
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/mol type="genomic RNA"
/isolate="HKU-65806"
/db_xref="taxon:231520"
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/isolate="G260"
/db_xref="taxon:231518"
/country="Hong Kong"
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Guan, Y. and Zheng, B.J.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.

1 (Dases 1 to 13471)
Guan, Y., Zheng, B.J., He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L., Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L., Chan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and Poon, L.L.M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (27-MAY-2003) Microbiology, The University of Hong Kong,
University Pathology Building, Queen Mary Hospital, Pokfulam Road,
Submitted (27-MAY-2003) Microbiology, The University of Hong Kong,
University Pathology Building, Queen Mary Hospital, Pokfulam Road,
Hong Kong, China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolation and characterization of viruses related to the SARS coronavirus from animals in southern China Science 302 (5643), 276-278 (2003)
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AY463060.1 GI:40457448

    13471
/organism="SARS coronavirus HKU-36871"

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                                                                               /organism="SARS coronavirus GZ43"
/mol type="genomic RNA"
/isolate="GZ43"
/db xref="taxon:231517"
/country="Hong Kong"
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/isolate="HKU-36871"
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SARS coronavirus HKU-36871
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AY304492.1 GI:34482143
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Guan, Y. and Zheng, B.J.
Direct Submission
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IETRLRKGGRTRCFGGCVFAYVGCYNKRAYWVPRASADIĞSGHTGITGDNVETLNBDL
LEILSREWYNINVODFHLAKBEYALILASFGARTAFITLIR KELDYKSFYTIVBGCGN
YKYTKGKPYKGAWNI GQQRSVLTPLCGFPSGQARGVTRSIFATLDAANHSI PDLQRAA
VTILDGISBGSLRLVDAMVYTSDLTNSVI İNAYVTGGLVQQTSQMLSNLLGTTVEKL
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DFLKATCEHCGTENLV I EGPTTCGYLPTNAVVKMPCPACQDPE I GPEHSVADYHNHSN
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NKALEMCI DQVTI AGAKLRSLNLGEVFIAQSKGLYRQCIRGKEQLQLLMPLKAPKEVT
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YCALSPGLLATNNVFRLKGGAPI KGVTFGEDTVWEVQGYKNVRI TFELDERVDKVINE
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ENFSSRMYCSFYPPDEEEDDAECEEEEIDETCEHEYGTEDDYQGLPLEFGASAETVR
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VRTQVY I AVNDKALYEQVVMDYLDNLKPRVEAPKQEEPPNTEDSKTEEKSVVOKPVDV
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ALKKCKSAFYVLPSEAPNAKEEILGTVSWNLREMLAHAEEARKLMPICMDVRAIMATI
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VVCKHCGQKTTTLTGVEAVMYMGTLSYDNLKTGVSIPCVCGRDATQYLVQQESSFVMM
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CLSGLDSLDSYPALETIQVTISSYKLDLTILGLAAEWVLAYMLFTKFFYLLGLSAIMQ
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QDGVTRDIISTDDCFANKHAGFDAWFSQRGGSYKNDKSCPVVAAIITREIGFIVPGLP
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SARS coronavirus ShanghaiOXC2
SARS coronavirus ShanghaiQXC2
Viruses; sRNAh positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.

1 (bases 1 to 29013)
Yuan, Z., Zhang, X., Hu, Y., Lan, S., Zhou, Z., Wang, H. and Wen, Y.
Analysis of SARS coronavirus genome in Shanghai isolates
Unpublished
2 (bases 1 to 29013)
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                                                                                                                                                                                                                                                                                                                                                                                                          Yuan, Z., Zhang, X., Hu, Y., Lan, S., Zhou, Z., Wang, H. and Wen, Y. Direct Submission
Direct Submission
Submitted (11-NOV-2003) Key Lab of Medical Molecular Virology, Shanghai Medical College, Fudan University, 138 Yi Xue Yuan Road, Shanghai 200032, P.R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="SARS coronavirus ShanghaiQXC2"
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/strain="ShanghaiQxC2"
/db_xref="taxon:258508"
join[186. .12734,12734. .208
/note="ribosomal slippage"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAR86774.1"
/db_xref="GI:40457449"
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GDATTAYANSVFNICQAVTANVNALLSTDGNKIADKYVRNLQHRLYECLYRNRDVDHE
FVEVEYAYLKGHERSMILIDDRAVCYRNSVAQGOLVASIKPRAVLYYONVPRASEAK
CWTETDLTKGFHERCSQHTMLVMCGDDYVYLEYPDESRILGAGCFUDDIVKNDSTLAN
ERFVSLLAIDAYPLTKHPNQEYADVFHLYLQYIRKLHDELTGHMLDMYSVMLTNDNTSR
YMEBEFYERAMYTPHTVLQAVGACVLANSOTSLRACGACIRREPECCKCYCHYLSTSHK
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                                                                                                                                                                                                                                                                                                                                     DVRQIAPGQTGVIADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNYKYRYLRHGKLRP
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SARS coronavirus LC2
SARS coronavirus LC2
Viruses; sRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
1 (bases 1 to 29350)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Indels
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SARS coronavirus LC2, complete genome.
AY394999
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                                                     product="spike"
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codon start=1
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KEYWORDS
SOURCE
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AY394999/c
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CONSRTM
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From independent foci of epidemic outbreak to large genomic alteration in late phase viruses: evolution of the SARS-coronavirus Unpublished to 29350)
                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 25; DB 14; Length 29350; Best Local Similarity 100.0%; Pred. No. 0.033; Matches 25; Conservative 0; Mismatches 0; Indels 0;
                                                                                                    The SARS epidemiology consortium of Guangdong
Direct Submission
Submitted (19-SEP-2003) Guangdong, China
Location/Qualifiers
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                                      JOURNAL REFERENCE SAUTHORS CONSRIM TITLE I JOURNAL FEATURES SOURCE
TITLE
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Search completed: May 16, 2005, 02:00:25 Job time : 597.656 secs

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
                  Copyright
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using sw model OM nucleic - nucleic search, May 15, 2005, 17:17:00 ; Search time 320.703 Seconds (without alignments) 461.466 Million cell updates/sec Run on:

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Scoring table:

IDENTITY NUC Gapop 10.0 , Gapext 1.0

4390206 seqs, 2959870667 residues Searched:

Total number of hits satisfying chosen parameters:

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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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geneseqn2003ds:* geneseqn2004as:* geneseqn2004bs:* geneseqn2003cs:* geneseqn2003bs:* geneseqn2001as:* geneseqn2001bs:* geneseqn2002as:* geneseqn2002bs:* geneseqn2003as: geneseqn2000s:* 10: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		d۴۰				
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
C 1	25	100.0	29751	12	ADJ39000	Adi39000 SARS coro
7	17.8	71.2	1533	12	ADN74528	Adn74528 Thale cre
m	17.8	71.2	1557	٣	AAC49448	Aac49448 Arabidops
4	17.8	71.2	1792	ო	AAC49462	Aac49462 Arabidops
S	17.8	71.2	1800	е	AAC41738	Aac41738 Arabidops
9	17.6	70.4	1362	4	AAF60956	Aaf60956 P. putida
7	17.2	68.8	654	œ	ACA21273	Aca21273 Prokaryot
60	17.2	68.8	5588	9	ABK63658	Abk63658 Rat segue
σ	17.2	68.8	66499	13	ABD33094	Abd33094 Murine ca
10	17	68.0	4359	8	ADA69739	Ada69739 Rice gene
11	17	68.0	54037	13	ABD33323	Abd33323 Murine ca
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. 17	16.8	67.2	2838	4	ABL16246	Abl16246 Drosophil
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20	16.8	67.2	110000	~	AAV30458 4	Continuation (5 of

Continuation (5 of	Aag55844 Acetobact	Aaq86876 Aat11R ge	Ade93875 Ixodes sc	Aah69833 Human cer	Abn60784 Human can	Aat83872 DNA encod	Aas57698 cDNA #374	Abk35379 Human cDN	Aca35711 Prokaryot	Aas51408 Klebsiell	Aca19360 Prokaryot	Aas54023 Klebsiell	Ach95348 Klebsiell	Aat27105 Yeast cal	Adh34512 cDNA enco	Aaz20018 Wheat 1,3	Adhl8989 Human cel	Aas03081 Human dia	Add78284 Human CGD	Abx63768 Human cDN	Adr07979 Full leng	Aax01052 Nucleotid	Ada02867 Mouse Sel	Adb72605 Mouse Sel
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7.2	56.4	4.	6.4	66.4	56.4	6.4	56.4	66.4	66.4	66.4	66.4	66.4	66.4	4.	4.	4.	4.	4.	66.4	5.4	4.0	56.4	6.4	4.
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21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

RESULT 1

small interfering RNA; siRNA; modified ribonucleotide; viral replication inhibition; hepatitis C virus; HCV; hepatitis C; antiinflammatory; hepatotropic; virucide; hepatitis A virus; hepatitis D virus; hepatitis E virus; Ebola virus; rotavirus; reovirus; poliovirus; human papilloma virus; metapneumoniavirus; coronavirus; viral infection; gene; ds. SARS coronavirus nucleotide sequence. ADJ39000/c ID · ADJ39000 standard; DNA; 29751 BP. (first entry) 06-MAY-2004 ADJ39000; TID STATE OF
SARS coronavirus. WO2004011647-A1.

05-FEB-2004.

25-JUL-2003; 2003WO-US023104.

26-JUL-2002; 2002US-0398605P.

(CHIR) CHIRON CORP.

WPI; 2004-143862/14.

Han J, Seo MY, Houghton M;

New RNase resistant small interfering RNA, useful for treating viral infections, e.g., hepatitis C, influenza virus or coronavirus infection.

Example 10; Fig 3; 74pp; English.

The present invention describes a small interfering RNA (siRNA) which comprises a modified ribonuclectide, where the siRNA is resistant to RNase and retains the ability to inhibit viral replication. Also described: (1) inactivating a virus in a patient; (2) making a modified siRNA that targets a nucleic acid sequence in a virus; (3) a double-

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hepatitis C virus (HCV); (4) inducting targeted RNA interference toward HCV in hepatic cells; (5) inhibiting replication of HCV; (6) a vector comprising a DNA segment encoding the RNA molecule; (7) a host cell comprising the vector of (6); (8) inhibiting replication of HCV in cells carrying HCV; (9) treating hepatitis C in a subject; (10) a modified signah molecule comprising a double-stranded RNA molecule of 10-30 nucleotides in length, which mediates RNA interference toward a target agent or virus and is linked to at least one receptor-binding ligand; and collecting targeted RNA interference in a patient. The modified siRNA molecules are useful for inactivating virus in mammalian cells. The siRNAs molecules are useful for treating hepatitis C virus, hepatitis B virus, hepatitis D virus, retrovirus, pollovirus, numan papilloma virus, metapneumoniavirus or coronavirus inflections. The metapneumoniavirus or coronavirus inflections. The metapneumoniavirus or coronavirus inflections. The metapods of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Altering plant characteristics, useful for producing plants for enzyme or pharmaceutical production comprises modifying in a plant, expression of one or more nucleic acids and/or modifying level or activity of one or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to a novel method for altering one or more plant characteristics. Specifically, it refers to identifying genes that are up
                                                                                                                                                                                                                                                                                                                                                            invention can be used to correct or compensate for cellular physiological abnormalities involved in conferring susceptibility to viral infections in patients and/or alleviate symptoms of a viral infection in patients. The present sequence represents the SARS coronavirus nucleotide sequence,
stranded RNA molecule of 10-30 nucleotides that inhibits replication of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 29751 BP; 8478 A; 5941 C; 6188 G; 9144 T; 0 U; 0 Other;
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growth regulator; animal feed product; thale cress;
cell wall biosynthesis; nitrogen metabolism; carbon metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match

100.0%; Score 25; DB 12; Length 29751;
Best Local Similarity 100.0%; Pred. No. 0.063;
Matches 25; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          is used in an example from the present invention.
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cc earler plant characteristics accordingly. The present invention describes to alter plant characteristics accordingly. The present invention describes generating transgenic plants for the production of growth regulators, centrally transgenic plants for the production of growth regulators, centrally transgenic plants for the production of growth regulators, central plant characteristics are selected from increased yield or blomass, enhanced survival capacity, stress tolerance, plant architecture or physiology, altered endoreduplication, biochemistry, signal corresponding wild type plants. Accordingly, these cach relative to the corresponding wild type plants. Accordingly, these sequences can also be useful as positive or negative selectable markers during transformation of cells or tissues. The identified genes play a cole in a variety of biological processes such as DNA replication, cell carling transcription factors. This polymuleotide sequence is thale cress cDNA repressed 1.3 fold or more in plants overexpressing the E2Fa/DPa
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90.5%;
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08-APR-1999;
16-APR-1999;
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06-MAY-1999;
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23 - JUL - 1999; 23 - JUL - 1999; 26 - JUL - 1999; 27 - JUL - 1999; 27 - JUL - 1999; 27 - JUL - 1999; 28 - JUL - 1999; 02 - AUG - 1999; 03 - AUG - 1999; 04 - AUG - 1999; 06 - AUG - 1999;	06-AUG-1999; 09-AUG-1999; 10-AUG-1999; 11-AUG-1999; 11-AUG-1999; 11-AUG-1999; 11-AUG-1999; 11-AUG-1999; 11-AUG-1999; 11-AUG-1999; 20-AUG-1999; 20-AUG-1999; 21-AUG-1999; 22-AUG-1999; 23-AUG-1999; 23-AUG-1999; 27-AUG-1999;	13-SEP-1999; 16-SEP-1999; 16-SEP-1999; 22-SEP-1999; 23-SEP-1999; 24-SEP-1999; 24-SEP-1999; 24-SEP-1999; 24-SEP-1999; 26-OCT-1999; 06-OCT-1999; 06-OCT-1999; 13-OCT-1999; 13-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 14-OCT-1999; 16-OCT-1999; 17-OCT-1999; 18-OCT-1999; 18-OCT-1999; 21-OCT-1999; 21-OCT-1999; 21-OCT-1999; 21-OCT-1999; 21-OCT-1999; 21-OCT-1999; 21-OCT-1999; 21-OCT-1999; 21-OCT-1999; 21-OCT-1999;
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9908-0135124P

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26 - MAX - 1999;
27 - MAX - 1999;
01 - JUN - 1999;
03 - JUN - 1999;
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14.-JUL-1999;
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                                                                                                              Score 17.8; DB 3; Length 1557; Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                               Arabidopsis thaliana DNA fragment SEQ ID NO: 61250.
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99US-0123180P
99US-012548B
99US-0126764P
99US-0126765P
99US-01267462P
99US-012874P
99US-0128714P
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99US-013048P
99US-0132468P
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99US-013248P
99US-0160981P.
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99US-0161404P.
99US-0161406P.
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Best Local Similarity 90.5
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
22-OCT-1999;
22-OCT-1999;
25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
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05-MAR-1999,
23-MAR-1999,
25-MAR-1999,
10-APR-1999,
01-APR-1999,
06-APR-1999,
06-APR-1999,
19-APR-1999,
19-APR-1999,
19-APR-1999,
23-APR-1999,
23-APR-1999,
23-APR-1999,
06-MAY-1999,
06-MAY-1999,
06-MAY-1999,
06-MAY-1999,
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14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
19-MAY-1999;
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PR 02-AUC-1999; 99US-0146386 P.

PR 02-AUC-1999; 99US-0146386 P.

PR 02-AUC-1999; 99US-0146386 P.

PR 02-AUC-1999; 99US-014638 P.

PR 02-AUC-1999; 99US-014638 P.

PR 02-AUC-1999; 99US-014312 P.

PR 02-AUC-1999; 99US-014811 P.

PR 11-AUC-1999; 99US-01481 P.

PR 11-AUC-1999; 99US-01481 P.

PR 11-AUC-1999; 99US-01481 P.

PR 11-AUC-1999; 99US-01481 P.

PR 12-AUC-1999; 99US-01481 P.

PR 12-AUC-1999; 99US-01481 P.

PR 12-AUC-1999; 99US-01481 P.

PR 20-AUC-1999; 99US-01440 P.

PR 20-AUC-1999; 9
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                                                                                                                                                                Gaps
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0
                                                                                                                    Ouery Match
71.2%; Score 17.8; DB 3; Length 1792;
Best Local Similarity 90.5%; Pred. No. 1.5e+02;
Matches 19; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana DNA fragment SEQ ID NO: 32954.
                                                                                                                                                                                                                                          1122 TGAACCAGGAAGCAGTATTAT 1142
                                                                                                                                                                                                      S TGAACCAAGACGCAGTATTAT 25
                                                                                                                                                                                                                                                                                                                                                AAC41738 standard; DNA; 1800 BP
99US-0161361P.
99US-0161920P.
99US-0161992P.
99US-0161993P.
99US-0162142P.
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99US-0123180P.
99US-0125784P.
99US-0126264P.
99US-0126785P.
99US-0126782P.
99US-0128234P.
99US-0128714P.
99US-0128714P.
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990S-0135629P.
990S-0136021P.
990S-0136392P.
990S-0136782P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana.
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
18-MAY-1999;
20-MAY-1999;
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9908-0147260P. 9908-014736P. 9908-014735P. 9908-014735P. 9908-014735P. 9908-0148735P. 9908-014811P. 9908-014811P. 9908-0149722P. 9908-0149722P. 9908-0149722P. 9908-0149722P. 9908-0149722P. 9908-0149722P. 9908-0149722P. 9908-015086P. 9908-015086P. 9908-0151086P. 9908-015233P. 9908-015339P. 9908-0155865P. 9908-0156865P. 9908-0156865P. 9908-0156865P. 9908-0156865P. 9908-0156865P. 9908-0156865P. 9908-0156865P. 9908-016691P. 9908-016091P. 9908-016091P. 9908-016091P. 9908-0161389P. 9908-0161389P. 9908-0161389P. 9908-0161389P. 9908-0161389P. 9908-0161389P. 9908-0161389P. 9908-0161389P. 9908-0161389P.	71.2%; Score 17.8; DB 3; Length 1800;
PR 05-AUG-1999; PR 06-AUG-1999; PR 06-AUG-1999; PR 06-AUG-1999; PR 06-AUG-1999; PR 12-AUG-1999; PR 13-AUG-1999; PR 13-AUG-1999	Query Match
990S - 0137528P . 990S - 0137528P . 990S - 0137724P . 990S - 0138640P . 990S - 0139640P . 990S - 0139642P . 990S - 0139452P . 990S - 0139460P . 990S - 0139460P . 990S - 0149453P . 990S - 0149545P . 990S - 014933P . 990S - 014433P . 990S - 0144332P . 990S - 0144332P . 990S - 0144332P . 990S - 0144333P . 990S - 0144333P . 990S - 0144332P . 990S - 0144333P . 990S - 0144333P . 990S - 0144338P . 990S - 0144338	99US-0147192P.
03 - JUN - 1999; 04 - JUN - 1999; 08 - JUN - 1999; 10 - JUN - 1999; 14 - JUN - 1999; 15 - JUN - 1999; 16 - JUN - 1999; 17 - JUN - 1999; 18 - JUN - 1999; 19 - JUN - 1999; 10 - JUN - 1999; 11 - JUN - 1999; 12 - JUN - 1999; 13 - JUN - 1999; 14 - JUN - 1999; 15 - JUN - 1999; 16 - JUN - 1999; 17 - JUN - 1999; 18 - JUN - 1999; 19 - JUN - 1999; 10 - JUN - 1999; 11 - JUN - 1999; 12 - JUN - 1999; 13 - JUN - 1999; 14 - JUN - 1999; 15 - JUN - 1999; 16 - JUN - 1999; 17 - JUN - 1999; 18 - JUN - 1999; 19 - JUN - 1999; 19 - JUN - 1999; 10 - JUN - 1999; 10 - JUN - 1999; 11 - JUN - 1999; 12 - JUN - 1999; 13 - JUN - 1999; 14 - JUN - 1999; 15 - JUN - 1999; 16 - JUN - 1999; 17 - JUN - 1999; 18 - JUN - 1999; 18 - JUN - 1999; 18 - JUN - 1999; 19 - JUN - 1999; 10 - JUN - 1999; 10 - JUN - 1999; 10 - JUN - 1999; 11 - JUN - 1999; 12 - JUN - 1999; 13 - JUN - 1999; 14 - JUN - 1999; 15 - JUN - 1999; 16 - JUN - 1999; 17 - JUN - 1999; 18 - JUN - 1999; 18 - JUN - 1999; 19 - JUN - 1999; 10 - JUN - 1999; 10 - JUN - 1999; 11 - JUN - 1999; 11 - JUN - 1999; 12 - JUN - 1999; 13 - JUN - 1999; 14 - JUN - 1999; 15 - JUN - 1999; 16 - JUN - 1999; 17 - JUN - 1999; 18 - JUN - 1999; 18 - JUN - 1999; 18 - JUN - 1999; 19 - JUN - 1999; 10 - JUN - 1999; 10 - JUN - 1999; 11 - JUN - 1999; 11 - JUN - 1999; 12 - JUN - 1999; 13 - JUN - 1999; 14 - JUN - 1999; 15 - JUN - 1999; 16 - JUN - 1999; 17 - JUN - 1999; 18 - JUN - 1999; 18 - JUN - 1999; 19 - JUN - 1999; 10 - JUN - 1999; 10 - JUN - 1999; 11 - JUN - 1999; 11 - JUN - 1999; 12 - JUN - 1999; 13 - JUN - 1999; 14 - JUN - 1999; 15 - JUN - 1999; 16 - JUN - 1999; 17 - JUN - 1999; 18 - JUN - 1999; 18 - JUN - 1999; 18 - JUN - 1999; 18 - JUN - 1	04-AUG-1999;
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Gaps

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Indels

4;

0; Mismatches

Conservative

20;

Matches

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This invention describes novel DNA sequences (I) for specific detection of Pseudomonas putida KT2440. The invention also describes (1) recombinant expression vector containing (I); (2) prokaryotic or recombinant expression vector containing (I); (2) prokaryotic or containing (I); (3) production of expression products by culturing cells of (2); (4) expression products, or their fragments, of (I) and synthetic proteins or peptides with the same sequences (A); (5) poly- or mono-clonal antibodies (Ab) that react specifically with (A); (6) hybridoma cells that produce the monoclonal Ab of (5); (7) transgenic plants that contain transformed or transfected cells of (2); (8) detecting KT2440 using a labeled (I) or Ab as probe; and (9) DNA chips carrying one or more (I). (I), and their fragments, are used as probes to detect and isolate full-length cDNAs and/or to amplify such cDNAs by polymerase chain reaction, and for production of transgenic plants. (I), or antibodies that recognize their expression products, are used for detecting the presence of KT2440, particularly in presence of other, even closely related, bacteria. KT2440
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      is one of the bacteria classified as safe, by the National Institutes of Health, for genetic engineering work, e.g. as microbial production strains, for biological remediation and as vaccine carriers. (I) are exclusive to KT2440 with no significant homology with sequences in other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New DNA sequences specific for Pseudomonas putida KT2440, useful as safe genetic engineering host, allow detection in presence of other related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bacteria (specifically the closely related pathogen P. aeruginosa).
Compared with other 'safe' bacteria, it has greater catabolic activity
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                         probe; amplification; vaccine carrier; biological remediation; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1362 BP; 316 A; 376 C; 382 G; 288 T; 0 U; 0 Other;
                                      Indels
90.5%; Pred. No. 1.5e+02; Mismatches 2;
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                                                                                                                                                                                                                                                                                                                                    P. putida KT2440-associated DNA ORF00268.
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MEDIZINISCHE HOCHSCHULE HANNOVER.
                                                                                                    1120 TGAACCAGGAAGCAGTATTAT 1140
                                                                             5 TGAACCAAGACGCAGTATTAT 25
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                                                                                                                                                                                                             AAF60956 standard; DNA; 1362 BP.
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                                                                                                                                                                                                                                                                                                                                                                         Transgenic plant; detection; microbial production strain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99DE-01035088.
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              Best Local Similarity 90.5
Matches 19; Conservative
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Score 17.6; DB 4; Length 1362; Pred. No. 1.8e+02;

70.4%;

Best Local Similarity

Query Match

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the foll antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are:

(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a gene in an operon required for the gene product or that has an activity against a biological pathway to required for proliferation, (7) identifying a compound that influences the activity of identifying a gene required for cellular proliferation or the biological pathway in which a proliferation required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profilling a compound; (8) expendict is overexpressed or underexpressed; (12) determining the extent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to which each of the strains is present in a culture or collection of strains, or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for howologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention relates to an isolated nucleic acid comprising any one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zyskind JW;
Xu HH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New antisense nucleic acids, useful for identifying proteins or scre
for homologous nucleic acids required for cellular proliferation to
isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     drug discovery programs, or for screening homologous nucleic acids
                                                                                                                                                                                                                                                                                                 ds; prokaryotic essential gene; cell proliferation;
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Forsyth RA,
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Yamamoto R,
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                        1237 CTGTTAACCAAGAAGCAGGCTTAT 1260
  25
2 CTGTGAACCAAGACGCAGTATTAT
                                                                                                                                                                                                                                                           Prokaryotic essential gene #2930
                                                                                                                                       BP.
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Carr GJ,
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06-SEP-2001; 2001US-00948993.
25-OCT-2001; 2001US-0342923P.
08-FEB-2002; 2002US-00072851.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-OCT-2001; 2001US-0342923P
08-FEB-2002; 2002US-00072851
06-MAR-2002; 2002US-0362699P
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                                                                                                                                     ACA21273 standard; DNA; 654
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Trawick JD,
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P-PSDB; ABU17403.
                                                                                                                                                                                                                                                                                                                                                           Bacillus anthracis.
                                                                                                                                                                                                                                                                                                                      drug design; gene.
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                                                                                                                                                                                                                                                                                               Antisense;
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Wall D,
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required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to methods for predicting toxic effects of compounds or the progression of these toxic effects by determining the global changes in gene expression in tissues or cells exposed to the toxin and comparing these to gene expression in unexposed tissues or cells. Also included are methods of predicting at least one toxic effect of a compound or progression of a toxic effect, preferably the hepatotoxicity of a compound, comprising detecting the level of expression in a tissue or cell sample exposed to the compound of two or more genes listed in the specification, where differential expression of the genes is indicative of at least one toxic effect or progression. The method can also be used to identify an agent which modulates the toxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat sequence differentially expressed in response to a hepatotoxin #1565.
                                                                                                                                                                                           Gaps
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                                                                                                                                                      Length 654;
                                                                                                                                                      Score 17.2; DB 8; Length 6 Pred. No. 2.6e+02; 0; Mismatches 3; Indels
                                                                                                                       Sequence 654 BP; 240 A; 89 C; 147 G; 178 T; 0 U; 0 Other;
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                                                                   electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                             476 GTGAATCAAGACGCATTATTT 497
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2001US-0290029P.
2001US-029545P.
2001US-0293336P.
2001US-0297457P.
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                                                                                                                                                       Query Match
Best Local Similarity 86.4%;
Matches 19; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissues or cells.
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06-JUN-2001;
13-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                   ABK63658;
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response and predict cellular pathways that a compound modulates in a cell. The methods utilise a set of at least two probes (on a solid support in kit form), where each of the probes comprises a sequence that specifically hybridises to a gene listed in the specification, a computer system comprising a database containing information identifying the expression level in a tissue or cell sample exposed to a hepatotoxin of a set of genes comprising at least two genes listed in the specification, and a user interface to view the information used to present information can a user interface to view the information used to present information clasted in the expression level in a tissue or cell of at least one gene listed in the specification. The method is useful for elucidating global changes in gene expression and for identifying toxicity markers in trissues or cell exposed to a known toxin. The genes may be used as tissues or cell exposed to a known toxin. The genes may be used as and gene expression information may be used as diagnostic markers for the prediction or identification of the physiological state of tissue or cell sample that has been exposed to a compound or agent. Hepatotoxicity is characterised by centrilobular necrosis and steatosis. The present sequence is an expressed sequence as (BST) or CDNA derived from a gene which is differentially expressed in response to a hepatotoxic agent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             associated (CA) nucleic acids encoding them. The invention also relates to a method for treating cancers involving administering to a patient an inhibitor of CAP, and a method of screening for anticancer activity in a potential drug involving providing a cell that expresses a CA gene, contacting a tissue sample derived from a cancer call with an anticancer drug candidate and monitoring the effect of the anticancer on expression of the CA gene. The CAP proteins are useful for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to cancer-associated proteins (CAP) and the cancer-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer-associated protein; CAP; cancer-associated gene; CA; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel human cancer associated protein encoded within open reading frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of cancer associated gene, useful as targets for diagnosing cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5588 BP; 1349 A; 1550 C; 1416 G; 1272 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 5588;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 17.2; DB 6;
Pred. No. 3.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene MD07-007.
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Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABD33094 standard; DNA; 66499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68.8%;
86.4%;
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Best Local Similarity 86.4
Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ds; cancer; cytostatic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABD33094;
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cancer associated with expression of a CAP protein in a test cell sample and for screening for a bloactive agent capable of modularing the activity of a CAP protein. The CA mucleic acids are useful for diagnosing cancer, involving determining the expression of a CA mucleic acid in a classure. This sequence repersents a murine CA gene of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
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                                                                                                                                                                 Sequence 66499 BP; 16137 A; 16098 C; 16364 G; 17399 T; 0 U; 501 Other;
                                                                                                                                                                                                                                            Gaps
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T, Zou G;
                                                                                                                                                                                              Score 17.2; DB 13; Length 66499;
Pred. No. 5.3e+02;
0; Mismatches 3; Indels 0;
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Whitham S, Xie Z, Zhu
                                                                                                                               ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                  4519 CTGTGACCCAAGACACAGTTTT 4540
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S, Tao Y,
                                                                                                                                                                                                                                                                                                                                                                                                          ADA69739 standard; DNA; 4359
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                                                                                                                                                                                                    68.8%;
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Matches 19; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-175290/17
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                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene;
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The invention relates to cancer-associated proteins (CAP) and the cancer-associated (CA) nucleic acids encoding them. The invention also relates to a method for treating cancers involving administering to a patient an inhibitor of CAP, and a method of screening for anticancer activity in a potential drug involving providing a cell that expresses a CA gene, contacting a tissue sample derived from a cancer cell with an anticancer drug candidate and monitoring the effect of the anticancer drug candidate and monitoring the effect of the anticancer drug candidate on expression of the CA gene. The CAP proteins are useful for detecting and for screening for a bioactive agent capable of modulating the activity of a CAP protein. The CA nucleic acids are useful for diagnosing cancer, involving determining the expression of a CA nucleic acid in a tissue. This sequence represents a murine CA gene of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mouse; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
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Pred. No. 6.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murine cancer-associated (CA) gene MD07-058,
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                                         3354 GATGGGAACGAAGACACATTATTAT 3378
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                                                                                                                                                                                                                                          ABD33323 standard; DNA; 54037
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80.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ds; cancer; cytostatic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus.
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ch 68.0%; Score 17; DB 8; Length 4359; 1 Similarity 80.0%; Pred. No. 4.4e+02; 20; Conservative 0; Mismatches 5; Indels

Best Local Similarity Matches 20; Conserv

Query Match

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ds; diagnosis; non-blood disease; solid tumor; gene expression; peripheral blood mononuclear cell; renal cell carcinoma; prostate cancer; head/neck cancer; differential expression.
                                                                                                                                                                                                                                                                                                                             are associated with Carcinomes. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vii) for inhibiting the activity of CAP; (vii) for treating carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CAP genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent
                                                                                                                                                                                          Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
                                                                                                                                                                                                                                                                                                               present invention relates to novel DNA and protein sequences which
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 68.0%; Score 17; DB 11; Length 73771; 80.0%; Pred. No. 6.7e+02; ive 0; Mismatches 5; Indels 0
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                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 1636; Opp; English.
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                  01-MAR-2002; 2002US-00087192
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nes 20; Conservative
                                                               (SAGR-) SAGRES DISCOVERY
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TREPICCHIO W L.
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STOVER J A.
SLONI D K.
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                                                                                                              Morris DW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
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                                                                                                              Cytostatic; carcinoma; lymphoma; cancer; murine; gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21903 GCTGTGAAACAAGACATTGTAATAT 21879
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                                                                 Mouse genomic sequence mCG22656
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                     18-NOV-2004 (first entry)
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Best Local Similarity
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                                                                                                                                                         Mus musculus.
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The invention relate to a method of diagnosing (M1) non-blood disease such as solid tumor by providing peripheral blood sample of human having non-blood disease, and comparing an expression profile of specific genes in the peripheral blood sample to reference expression profile of the genes, where each of the genes is differentially expressed in peripheral blood amonuclear cells (PBMCs) of patients having the disease as compared to PBMCs of normal humans. The method is useful for diagnosing non-blood disease such as solid tumor. The solid tumor is chosen from peripheral blood sample comparises enriched PBMCs. The peripheral blood sample (claimed). (M1) is useful for identifying genes that are differentially expressed in peripheral blood samples is a hole blood sample (claimed). (M1) is useful for identifying genes that are differentially expressed in peripheral blood samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      isolated at different stages of progression, development or treatment of RCC and/or other solid tumors. This sequence corresponds to a gene that is differentially expressed and detected by the method of the invention. (Note: this sequence is not given as part of the printed specification but was obtained from WIPO in electronic format at
                                                                                                                                                                  differential expression profile of specific genes in peripheral blood sample of subject with reference expression profile of specific genes
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                                                                                                                                     Diagnosing non-blood disease such as solid tumor, involves comparing differential expression profile of specific genes in peripheral blood
  Dorner A, Stover JA;
  Trepicchio WL,
                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 68; 350pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ftp.wipo./pub/published_pct_sequences)
Burczynski ME,
                                                                                 WPI; 2004-460799/43.
Twine NC,
Sloni DK;
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Gaps °, Score 17; DB 12; Length 126990; Pred. No. 7.3e+02; 0; Mismatches 5; Indels 0; 108520 GCTGTGAACAGAGACTCATTGTTAT 108544 25 1 GCTGTGAACCAAGACGCAGTATTAT Query Match
Best Local Similarity 80.0°
Matches 20; Conservative ઠે 셤

68.0%; 80.0%;

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ABL16247 standard; DNA; 780 BP. 26-MAR-2002 (first entry) ABL16247; RESULT 15 ABL16247/c

Drosophila; developmental biology; cell signalling; insecticide; Drosophila melanogaster genomic polynucleotide SEQ ID NO 214. pharmaceutical; gene; ds Drosophila melanogaster. WO200171042-A2 THE REAL REAL PROPERTY OF A SECTION OF THE PROPERTY OF THE PRO

23-MAR-2001; 2001WO-US009231 27-SEP-2001

23-MAR-2000; 2000US-0191637P. 11-JUL-2000; 2000US-00614150. (PEKE) PE CORP NY.

Adams M, Venter JC,

WPI; 2001-656860/75.

Myers EW;

PWD,

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New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABBS7777-ABB72072). The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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Pred. No. 4.2e+02;
0; Mismatches 2; Indels (
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                                            Claim 1; SEQ ID NO 214; 21pp + Sequence Listing; English.
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4463, Ap 13478, Ap 1285, Appl 12851, A 11890, A 3, Appl 3, Appli 14952, A 12883, A 15496, A

4346, Ap 13, Appl

Perfect score:

Run on:

Sequence:

Scoring table:

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Sequence 12953, Application US/09949016

Patent No. 6812339

GENERAL INPORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-03

PRIOR PLING DATE: 2000-0-08

PRIOR PRILING DATE: 2000-0-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 12953
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 12954, Application US/09949016
Sequence 12954, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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Sequence 14433,
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Pred. No. 1.2e+02;
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US-09-463-402-5
US-09-889-572-3
US-09-889-572-3
US-09-463-402-13
US-09-49-016-13478
US-09-949-016-13478
US-09-949-016-13478
US-09-949-016-13890
US-09-949-016-12851
US-09-949-016-12851
US-09-949-016-12851
US-09-949-016-12883
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US-09-949-016-12953
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Best Local Similarity 83.3%;
Matches 20; Conservative
                          NAME/KEY: misc_feature
  ORGANISM: Human
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Sequence 12054, Ap
Sequence 16054, A
Sequence 17567, A
Sequence 17567, A
Sequence 11188, A
Sequence 11809, A
Sequence 11809, A
Sequence 1, Appli
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11926, A
3, Appli
17539, A
335, App
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(cgn2_6/ptodata/1/ina/5A_COMB.seq:*

(cgn2_6/ptodata/1/ina/5B_COMB.seq:*

(cgn2_6/ptodata/1/ina/6A_COMB.seq:*

(cgn2_6/ptodata/1/ina/6B_COMB.seq:*

(cgn2_6/ptodata/1/ina/RecTUS_COMB.seq:*

(cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
                5.1.6
Compugen Ltd.
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US-09-949-016-126054
US-09-949-016-126054
US-09-949-016-12609
US-09-949-016-13118
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US-09-1314-570-3
US-09-131-143
US-09-132-9
US-09-949-016-2939
US-08-323-9
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US-09-949-016-59665
US-09-328-352-744
US-09-543-681A-171
                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                        1202784 segs, 818138359 residues
                                                                                                                                                                                  gctgtgaaccaagacgcagtattat 25
                GenCore version
Copyright (c) 1993 - 2005
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                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                     OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                            IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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25
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Maximum DB seq length: 200000000
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Result No.

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Sequence 12609, Application US/09949016

Sequence 12609, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CLOON 1307

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-00-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRESEERCE

SOFTWARE

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Sequence 17567. Application US/09949016;
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CL001307
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Best Local Similarity 80.0%; Pred. No. 2.8e+02;
Matches 20; Conservative 0; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68.0%; Score 17; DB 4; Le 80.0%; Pred. No. 2.4e+02; iive 0; Mismatches 5;
; PRIOR FILING DATE: 2000-10-20; PRIOR APPLICATION NUMBER: 60/237,768; PRIOR FILING DATE: 2000-10-03; PRIOR FILING DATE: 2000-09-08; PRIOR FILING DATE: 2000-09-08; NUMBER OF SEQ ID NOS: 207012; SOFTWARE: PastSEQ for Windows Version 4.0; SEQ ID NO 16054; LENGTH: 51336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35840 GCTGTGATTCAGGAGGCAGAATTAT 35864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32583 GTTGTGAACTGAGACCCAGGATTAT 32607
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| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16054
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| LOCATION: (1)...(109025)

| OTHER INFORMATION: n = A,T,C or G

US-09-949-016-12609
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 80.0%
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NAME/KEY: misc_feature
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US-09-949-016-17567
                                                                                                                                                                                                                                                                                                                                ORGANISM: Human
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APPLICANT: Keith Weinstock et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERBNE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
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; OTHER INFORMATION: Identity of nucleotide sequences at the above locations are unkno
US-09-248-796A-8219
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US-09-049-016-16054

Squence 16054, Application US/09949016

Squence 16054, Application US/09949016

Squence 16054, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT FILING DATE: 2000-04-14

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755
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   PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASLSEQ for Windows Version 4.0
SEQ ID NO 12954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7003 GCTGGGAACCCAGGCGCAGTATCA 7026
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PRIOR FILING DATE: 1998-02-13
PRIOR PILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 8219
LENGTH: 357
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                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (1)...(46492)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Candida albicans
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Best Local Similarity 80.0°
Matches 20; Conservative
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Matches 20; Conservative
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US-09-248-796A-8219
                                                                                                                                                                                                                                                                                                                                ORGANISM: Human
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AALII AND ALUI RESTRICTION ENDONUCLEASE AND METHYLASE AND RELATED METHOD FOR OVEREXPRESSING RESTRICTION
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APPLICANT: Rosenthal, Andre
APPLICANT: Freiberg, Christoph
APPLICANT: Pereiberg, Christoph
APPLICANT: Pereit, Xavier Philippe
APPLICANT: Broughton, William John
TITLE OF INVENTION: Genomic Sequence of Rhizobium SP. NGR 234 Symbiotic
Parent No. 6475793
TITLE OF INVENTION: Plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Sequence 3, Application US/08134570;
Patent No. 5405768;
GENERAL INFORMATION:
APPLICANT: Xu, Shuang-yong
APPLICANT: NWanko, Donald O.
APPLICANT: Porney, Julie A.
APPLICANT: Zhang, Bohong
TITLE OF INVENTION: METHOD FOR CLONING AND PRODUCING THE
TITLE OF INVENTION: Aatil AND Alui RESTRICTION ENDONUCLEASE;
TITLE OF INVENTION: AND RELATED METHOD FOR OVEREXPRESSING RE
TITLE OF INVENTION: ENDONUCLEASES
NUMBER OF SEQUENCES: 16
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                                                                                                                                                                                                                                                                                                                                                             Score 16.8; DB 4;
Pred. No. 3.5e+02;
0; Mismatches 2;
            PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 11809
LENGURH: 116425
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CURRENT APPLICATION NUMBER: US/09/214,808A
CURRENT FILING DATE: 199-06-22
PRIOR APPLICATION NUMBER: PCT/IB97/00950
PRIOR FILING DATE: 1997-07-10
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     2000-04-14
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90.0%;
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SOFTWARE: PatentIn Ver. 2.1
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Best Local Similarity
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Matches 18; Conserv
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                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                  US-09-949-016-11809
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LENGTH: 536165
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; Sequence 13118, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; FILE REFERENCE: CLOON 307
; CURRENT FILING DATE: 2000-04-14
    PRIOR PILING DATE: 2000-10-20
; PRIOR PILING DATE: 2000-10-03
; PRIOR PILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-0-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTMARE: FESTERORY
; MUMBER OF SEQ ID NOS: 207012
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Sequence 11809, Application US/09949016

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016
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Pred. No. 3.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 109025;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 68.0%; Score 17; DB 4; I Best Local Similarity 80.0%; Pred. No. 2.8e+02; Matches 20; Conservative 0; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                 CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PELICATION NUMBER: 60/237,768
PRIOR PELICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT APPLICATION NUMBER: US/09/949,016
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17567
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Best Local Similarity 90.0°
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
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                                                                                                                                                                                                                                      SEQ ID NO 17567
LENGTH: 109025
                                                                                                                                                                                                                                                                                         TYPE: DNA
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GENERAL INFORMATION:

APPLICANT: GATY Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
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APPLICANT: Huang, Laigiang
APPLICANT: Cyert, Martha S.
TITLE OF INVENTION: Calcineurin Interacting Protein Compositions
TITLE OF INVENTION: and Methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Deblinger & Associates
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  Indels
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MEDIUM TYPE: Floppy disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATE:

APPLICATION NUMBER: US/08/328,322

FILING DATE: 24-OCT-1994

CLASSIPICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Sholtz, Charles K.

REGISTRATION NUMBER: 98,615

REFERENCE/POCKET NUMBER: 8600-0151.10

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
66.4%; Score 16.6; DB 4;
Best Local Similarity 82.6%; Pred. No. 2e+02;
Matches 19; Conservative 0; Mismatches 4;
  4.
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: Dehlinger & Associates
350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1531 GCAATGACGCAAGACGCAGTATT 1509
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; Sequence 1143, Application US/09489039A
; Patent No. 6610836
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                                                    2 CTGTGAACCAAGACGCAGTATTA 24
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Patent No. 5723436
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TELEPAX: (415) 324-0860
INFORMATION FOR SEQ ID NO: 18:SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 1812 base pairs
nucleic acid
19; Conservative
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     Matches
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US-09-248-796A-6254/C
US-09-248-796A-6747137
Sequence 6254, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
TITLE OF INVENTION: NUCLEIC ACID AND ANINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN TITLE OF INVENTION: NUCLEIC ACID AND THERAPEUTICS
FILE REFERENCE: 107196-132
FILE REFERENCE: 107196-132
FRIOR FILING DATE: 1998-02-12
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-08-13
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
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  CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS
ADDRESSEE: CUSHMAN
STREET: 130 WATER STREET
CITY: BOSTON
                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/134,570
FILING DATE: 10-08-93
CLASSIFICATION: A35
PRIOR DATE: 0.08-93
CLASSIFICATION: DATA:
APPLICATION NUMBER: US 07/909947
FILING DATE: 07-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: CORLESS, PETER F.
REGISTRATION NUMBER: 33,860
REFERENCE/POCKET NUMBER: 44,891-CIP
TELEFPAN: (617) 523-3400
TELEFPAN: (617) 523-6440
TELEFPAN: (617) 523-6440
TELEFAN: (617) 523-6440
TELEFAN: (617) 523-6440
TELEFAN: (617) 523-6440
TELEFAN: CARACTERISTRE UR
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: unknown
                                                                                                                             MASSACHUSETTS
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Best Local Similarity
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LENGTH: 1455
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66.4%; Score 16.6; DB 1; Length 1812;
Best Local Similarity 82.6%; Pred. No. 2.1e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,322
FILING DATE: 24-OCT-1994
CLASSIFTCATION NUMBER: P38,615
REGISTRATION NUMBER: P38,615
REGISTRATION NUMBER: P38,615
REGISTRATION NUMBER: 9600-0151.10
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (415) 324-0860
TELEFRAX: (415) 324-0860
TELEFRAX: (415) 324-0860
TELEFRAX: (415) 324-0860
TELEFRAX: (415) 324-080
TELEFRAX: (415) 324-0860
                                                                                                                                             DNA fragment containing CNA1deltaC coding sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Huang, Laiqiang
APPLICANT: Cyert, Martha S.
TITLE OF INVENTION: Calcineurin Interacting ITILE OF INVENTION: and Methods
NUMBER OF SEQUENCES: 23
CORRESPONDENCES. 23
CORRESPONDENCE ADDRESSE:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 1964 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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286..1944
                                                                                                                                                                                                                                       286..1812
                                                                                        ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
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INDIVIDUAL ISOLATE:
INDIVIDUAL ISOLATE:
                                             MOLECULE TYPE: DNA HYPOTHETICAL: NO
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GENERAL INFORMATION:
                                                                                                                                                                                                              NAME/KEY: CDS
STRANDEDNESS:
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STRANDEDNESS:
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US-08-328-322-18
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66.4%; Score 16.6; DB 1; Length 1964;

Query Match

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Sequence 2614, Application US/09949016
Sequence 2614, Application US/09949016
Pacent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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                        4; Indels
Best Local Similarity 82.6%; Pred. No. 2.1e+02; Matches 19; Conservative 0; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09:08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.0
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                                                                  3 TGTGAACCAAGACGCAGTATTAT 25
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Job time: 97.5547 secs
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ORGANISM: Human
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                                       GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 2475, Ap	Sequence 16, Appl	Sequence 7, Appli	Sequence 11, Appl	Sequence 3, Appli	Sequence 5, Appli	Sequence 6, Appli	Sequence 4, Appli	Sequence 7, Appli	Sequence 15, Appl	Sequence 1, Appli
ΙD	US-10-808-187-2475	US-10-699-936-16	US-10-699-936-7	US-10-699-936-11	US-10-889-447-3	US-10-889-447-5	US-10-889-447-6	US-10-889-447-4	US-10-889-447-7	US-10-839-729-15	US-10-827-757-1
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US-10-889-447-8 US-10-699-936-1 US-10-689-447-9 US-10-689-936-3 US-10-689-936-3 US-10-689-936-3 US-10-689-936-3 US-10-689-187-16 US-10-808-187-16 US-10-808-187-1590 US-10-808-187-16631 US-10-626-879-67 US-10-626-879-67 US-10-626-879-67 US-10-626-879-67 US-10-626-879-67 US-10-626-879-67 US-10-425-114-6765 US-10-425-114-14784 US-10-425-118-1899 US-10-425-118-1899 US-10-282-128A-9143 US-10-282-128A-9143	DE US/10808187 D9009A1 PH S. M. FUNG AN HUNG A
100.0 29727 19 100.0 29727 19 100.0 29736 19 100.0 29736 19 100.0 29742 19 100.0 29742 19 100.0 29742 19 100.0 29742 19 100.0 29742 19 100.0 29742 19 100.0 29742 19 100.0 29742 19 100.0 29751 19 100.0	ESULT 1 Sequence 2475, Application US/108081 Publication No. US2005000909A1 GENERAL INFORMATION APPLICANT: PERRIS, JOSEPH S. M. APPLICANT: YUEN, KWOK YUNG APPLICANT: TOWN, IIT MAN APPLICANT: NICHOLLS, JOHNSTIC TITLE OF INVENTION: A DIAGNOSTIC AS TITLE OF INVENTION: RESPIRATORY S) FILE REFERENCE: V9661.0078 CURRENT APPLICATION NUMBER: 60/457, 73 PRIOR APPLICATION NUMBER: 60/457, 73 PRIOR PILING DATE: 2003-03-24 PRIOR PILING DATE: 2003-03-69 PRIOR PILING DATE: 2003-04-03 PRIOR PILING DATE: 2003-04-08 PRIOR PILIN
112 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	SULT 1 1-10-808-187-2475 Sequence 2475, Application GENERAL INFORMATION: US20050099 GENERAL INFORMATION: US20050099 APPLICANT: PEIRIS, JOSEPH APPLICANT: PEIRIS, JOSEPH APPLICANT: CHAN, KWOK HUJ APPLICANT: OF LIVENLES, JOH TITLE OF INVENTION: A DIAA TITLE OF INVENTION: RESP: TITLE OF INVENTION: RESP: CURRENT APPLICATION NUMBER: PRIOR FILING DATE: 2003-0. PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PRIOR PLILING DATE: 2003-0. PRIOR PLILING DATE: 2003-0. PRIOR PLILING DATE: 2003-0. PRIOR FILING DATE: 2003-0. PRIOR PLILING DATE: 2003-0. PRIOR PLILING DATE: 2003-0. PRIOR PLILING DATE: 2003-0. PRIOR FILING DATE: 2003-0. PRIOR PLILING DATE: 2003-0. PRIOR FILING DATE: 2003-0.
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1.0 Sequence 11, Application US/1069936
1.0 Sequence 11, Application No. US20050095582A1
1.0 GENERAL INFORMATION:
1.0 Sequence 11, Application No. US20050095582A1
1.0 GENERAL INFORMATION:
1.0 Sequence 11, Application No. US2005009558A1
1.0 Septicant: Gallim-Ross, Laura
1.0 Applicant: Taylor, Jill
1.0 Applicant: Wentworth, David R.
1.0 Applicant: Wentworth, Joseph D.
1.0 TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
1.0 TITLE OF INVENTION: Syndrome Coronavirus
1.0 FILE REFERENCE: DHI-07966
1.0 CURRENT APPLICATION NUMBER: US/10/699,936
1.0 CURRENT FILING DATE: 2003-11-03
1.0 NUMBER OF SEQ ID NOS: 87
1.0 SOFTWARE: Patentin version 3.2
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Sequence 3, Application US/10889447

Publication No. US20050075307A1

GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
APPLICANT: Jain, Ravi
TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
FILE REFERENCE: RTS-0685US
CURRENT APPLICATION NUMBER: US/10/889,447

CURRENT FILING DATE: 2004-07-12

PRIOR APPLICATION NUMBER: 60/486,670

PRIOR PLING DATE: 2003-07-12

NUMBER OF SEQ ID NOS: 241

SOFTWARE: FaatSEQ for Windows Version 4.0
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                       Length 2304;
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                       DB 19;
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Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 25; Conservative 0; Mismatches
                       Query Match 100.0%; Score 25; DB 19
Best Local Similarity 100.0%; Pred. No. 0.039;
Matches 25; Conservative 0; Mismatches
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                                                                                                                                                          921 GCTGTGAACCAAGACGCAGTATTAT 897
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US-10-699-936-16/C
US-10-699-936-16/C
is Sequence 16, Application US/1069936
is Publication No. US20050095582A1
is GENERAL INFORMATION:
is APPLICANT: Gillim-Ross, Laura
is APPLICANT: Taylor. Juli
is APPLICANT: Scholl, David R.
is APPLICANT: Wentworth, David E.
is APPLICANT: Wentworth, David E.
is APPLICANT: Oplick, Joseph D.
is TITLE OF INVENTION: Syndrome Coronavirus
is TITLE OF INVENTION: Syndrome Coronavirus
is TITLE OF INVENTION: Syndrome Coronavirus
is TITLE OF INVENTION: US/10/699,936
is CURRENT FILING DATE: 2003-11-03
is NUMBER OF SEQ ID NOS: 87
is SOFTWARE: PatentIn version 3.2
is SEQ ID NO 16
is LINCTH: 1620
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APPLICANT: Taylor, Jill
APPLICANT: Scholl, David R.
APPLICANT: Scholl, David R.
APPLICANT: Wentworth, David E.
APPLICANT: Jollick, Joseph D.
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
TITLE OF INVENTION: Syndrome Coronavirus
TITLE OF INVENTION: Syndrome Coronavirus
TITLE OF INVENTION: 107986
CURRENT APPLICATION NUMBER: US/10/699,936
CURRENT PILING DATE: 2003-11-03
NUMBER OF SEQ ID NOS: 87
SEQ ID NO 7
LENGTH: 2304
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100.0%; Score 25; DB
Best Local Similarity 100.0%; Pred. No. 0.0
Matches 25; Conservative 0; Mismatches
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; ORGANISM: SARS-COV Shanghai LY
US-10-699-936-7
                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS: 2476
SOFTWARE: Patentin ver. 3.2
SEQ ID NO 2475
LENGTH: 25
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; ORGANISM: SARS-COV ZJ-HZ01
US-10-699-936-16
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US-10-699-936-7/C
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Query Match
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 25; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                APPLICANT: Jain, Ravi
TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
FILE REFERENCE: RTS-069LMS: US/10/889,447
CURRENT APPLICATION NUMBER: US/10/889,447
CURRENT FILING DATE: 2004-07-12
PRIOR PRILING DATE: 2003-07-12
NUMBER OF SEQ ID NOS: 241
SOFTWARE: FASESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Jain, Ravi
TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
FILE REFERENCE: R72-0685US
CURRENT APPLICATION NUMBER: US/10/889,447
CURRENT FILING DATE: 2004-07-12
PRIOR APPLICATION NUMBER: 60/486,670
PRIOR FILING DATE: 2003-07-12
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TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 29430
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OTHER INFORMATION: n is any nucleotide
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COTHER INFORMATION: n is any nucleotide
US-10-889-447-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 15, Application US/10839729; Publication No. US20050002953A1; GENERAL INFORMATION:
Sequence 4, Application US/10889447
Publication No. US20050075307A1
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7, Application US/10889447; Publication No. US20050075307A1; GENERAL INFORMATION: APPLICANT: Bennett, C. Frank
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Best Local Similarity 100.0
Matches 25; Conservative
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US-10-839-729-15/c
                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 4
LENGTH: 29291
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                                                                                                                                                                                           APPLICANT: Bennett, C. Frank
APPLICANT: Jain, Ravi
APPLICANT: Jain, Ravi
APPLICANT: Jain, Ravi
TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
FILE REFERENCE: RIS-6685US
CURRENT APPLICATION NUMBER: US/10/889,447
CURRENT FILING DATE: 2004-07-12
PRIOR PILING DATE: 2004-07-12
NUMBER OF SEQ ID NOS: 241
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 28920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/10889447

Publication No. US20050075307A1

GENERAL INFORMATION:

APPLICANT: Bennett, C. Frank

APPLICANT: Jain, Ravi

TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION

FILE REFERENCE: RTS-0685US

CURRENT APPLICATION NUMBER: US/10/889,447

CURRENT FILING DATE: 2004-07-12

PRIOR FILING DATE: 2004-07-12

NUMBER OF SEQ ID NOS: 241

SOFTWARE: FASTSEQ for Mindows Version 4.0
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100.0%; Score 25; DB 19; Length 28920;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 25; Conservative 0; Mismatches 0; Indels 0;
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23399 GCTGTGAACCAAGACGCAGTATTAT 23375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: SARS coronavirus isolate BJ03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: SARS coronavirus isolate BJ04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GCTGTGAACCAAGACGCAGTATTAT 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: n is any nucleotide US-10-889-447-5
                                                                                                                        Sequence 5, Application US/10889447
Publication No. US20050075307A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
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LENGTH: 28920
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US-10-889-447-4/C
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RESULT 7

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LOCATION:

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GENERAL INFORMATION:
APPLICANT: Gillim-Ross, Laura
APPLICANT: Taylor, Jill
APPLICANT: Taylor, Jill
APPLICANT: Scholl, David R.
APPLICANT: Scholl, David R.
APPLICANT: Wentworth, David E.
APPLICANT: O'DILICK, JOSEPH D.
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
TITLE OF INVENTION: Syndrome Coronavirus
FILE REFERENCE: DHI-07986
CURRENT APPLICATION NUMBER: US/10/699,936
CURRENT FILING DATE: 2003-11-03
NUMBER OF SEQ ID NOS: 87
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                                                     Length 29727;
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Sequence 17, Application US/10839729

Sequence 17, Application US/10839729

Publication No. US20080002953A1

GENERAL INFORMATION:

APPLICANT: Jens Herold

TITLE OF INVENTION: AND METHODS OF USE

FILE REFERENCE: BIOBANK.013A

CURRENT APPLICATION NUMBER: US/10/839,729

CURRENT FILING DATE: 2004-05-04

PRIOR PILING DATE: 2003-05-06
                                                     Query Match 100.0%; Score 25; DB 19; Length 2 Best Local Similarity 100.0%; Pred. No. 0.061; Matches 25; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                 28286 GCTGTGAACCAAGACGCAGTATTAT 28262
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
                                                                                                                                                     1 GCTGTGAACCAAGACGCAGTATTAT 25
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; Sequence 1, Application US/10699936
; Publication No. US20050095582A1
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US-10-839-729-17
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Best Local Similarity
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          US-10-889-447-8
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Publication No. US2005004071A1
Publication No. US2005004071A1
Publication No. US2005004071A1
Publication No. US2005004071A1
APPLICANT: Comper, Wayne
TITLE OF INVENTION: Charged Polysaccharides Resistant To Lysosomal Degradation During
TITLE OF INVENTION: Kidney Filtration And Renal Passage And Their Use To Treat Or
TITLE OF INVENTION: Prevent Infection By Coronaviruses
FILE REFERENCE: 11213-007-999
CURRENT PAPLICATION UNMBER: US/10/827,757
CURRENT FILING DATE: 2004-04-02
PRIOR APPLICATION NUMBER: 60/464,294
PRIOR FILING DATE: 2003-04-21
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Query Match

Best Local Similarity 100.0%; Pred. No. 0.061;

Matches 25; Conservative 0; Mismatches 0; Indels 0;
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Publication No. US20050075307A1

GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
FILE REFRENCE: R2-0685US
CURRENT APPLICATION NUMBER: US/10/889,447

CURRENT FILING DATE: 2004-07-12

PRIOR FILING DATE: 2003-07-12
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 29727
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 29727
TITLE OF INVENTION: AND METHODS OF USE FILE REFERENCE: BIOBANK.013A CURRENT APPLICATION NUMBER: US/10/839,729 CURRENT FILING DATE: 2004-05-04 PRIOR APPLICATION NUMBER: 60/468703 PRIOR FILING DATE: 2003-05-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GCTGTGAACCAAGACGCAGTATTAT 25
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SOFTWARE: Patentin version 3.2
SEQ ID NO 1
LENGTH: 29727
                                                                                                                                                                                                                                                ; TYPE: DNA; ORGANISM: SARS Coronavirus
US-10-839-729-15
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US-10-827-757-1/c
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RESULT 15
US-10-889-447-9/C
i Sequence 9, Application US/10889447
; Publication No. US20050075307A1
; GENERAL INFORMATION:
i APPLICANT: Bennett, C. Frank
; APPLICANT: Jain, Ravi
TITLE OF INVENTION MUMBER: US/10/889,447
; CURRENT APPLICATION NUMBER: US/10/889,447
; CURRENT PILING DATE: 2003-07-12
; PRIOR APPLICATION NUMBER: 00/486,670
; PRIOR PILING DATE: 2003-07-12
; NUMBER OF SEQ ID NOS: 241
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 29736
; TYPE: DNA
; ORGANISM: SARS coronavirus CUHK-W1
US-10-889-447-9

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QUARTY MATCh

RESULT OF SEQ ID NO 9
; CORGANISM: SARS CORONAVIRUS CUHK-W1
US-10-889-447-9

QUARTY MATCH

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Search completed: May 16, 2005, 14:33:50 Job time: 1186.16 secs

28271 GCTGTGAACCAAGACGCAGTATTAT 28247

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Title: Perfect score:

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Minimum I Maximum I

Database

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CC408519 831 bp DNA linear GSS 19-MAY-2003 PUHJX26TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa468E04,
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BE622031 601440686
GG340017 OGODUGATH
AL305465 Tetracodon
BX842260 BX848260
AL165996 Tetracodon
AK084409 Mus muscu
AK085687 Wms muscu
CNG30835 taf52a10.
CN775412 tae81a08.
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    (bases 1 to 831)

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/clone lib="ZM 0.6 1.0 KB"
/note="Vector: pCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
CoT selected genomic DNA library"
                                                      AGENCOURT
CM2-CT031
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602351894
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CD180673 N
CE173136 t
CG094594 I
CK004840 A
                                                                        AW363138 CE100367 t BG122758 EBH060036 I CK764779 EBE507723 I
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9712 Medical Center Drive, Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                   CG094594
CK004840
AWAG1313
CK1003131
BG122758
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CK7640723
AW350543
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CG340017
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AK085687
CN630835
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Unpublished (2003)
Other GSSs: PUHJX26TB
Contact: Cathy Whitelaw
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Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genomic survey sequence
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CC408519.1 GI:30888609
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larity 88.0%;
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AZ880688 ZM0152F11
CG853284 ZMMBBD035
CN781966 ESTW0061
AZ122567 RPC1-23-2
BZ618666 igg2b07.b
CG137686 PUKCM44TD
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CG116875 PUKBP30TB
CN52254 Lea17c11.
AZ999859 ZM0287F19
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BZ880491 CH240_251
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AQ338179 HS Z215 B
BM891424 8am55908.
AZ025048 RPC1-23-3
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                                                                                                                       00:01:20 ; Search time 2823.44 Seconds (without alignments) 337.038 Million cell updates/sec
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Compugen Ltd.
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Copyright (c) 1993 - 2005
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Listing first 45 summaries
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AZ122567
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EST 06-DEC-2002 Beta vulgaris

KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

ACCESSION VERSION

DEFINITION CK302404/c

RESULT 2

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AZ850688 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCZM0152F11 R, genomic survey sequence.
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                                                                                                                                                                                          Beta vulgaris

Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;

Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Caryophyllales; Magnollophyta; eudicotyledons; core eudicots;

Caryophyllales; Amaranthaceae; Beta.

1 (Dases 1 to 955)

Herwig, R., Schulz, B., Weisshaar, B., Hennig, S., Steinfath, M.,
and Radelof, U.

Construction of a 'unigene' CDNA clone set by oligonucleotide

Eingerprinting allows access to 25 000 potential sugar beet genes

Plant J. 32 (5), 845-857 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SP6-SB11-CCACGCGTCCG-Sprime-cDNA-polyA-CC-Not1-T7; Note: Sequencing granted in the context of the GAB1-Beet project, local P1: Dr. Katharina Schneider, coordinator: Prof. Christian Jung; Sequence submission managed by RZPD/GAB1-Primary database: http://gabi.rzpd.de"
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Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Beta vulgaris"
/mol_type="mRNA"
/cultivar="KWS2320 (double haploid, monogerm breeding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Weisshaar B
ADIS DNA core facility at MPIZ
MAX-Planck-Institute for Plant Breeding Research
Carl-von-Linne Weg 10, 50829 Koeln, Germany
Fax: 00492215062851
Email: weisshaa@mpiz-koeln.mpg.de
Insert Length: 955 Std Brror: 0.00
Insert Length: 955 Std Brror: 0.00
Seg primer: SP6; CATACGATTAGGTGACACTATAG.
Location/Qualifiers
BQ590872 955 bp mRNA linear
E012599-024-018-D14-SP6 MPIZ-ADIS-024-storage root
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                                                      cDNA clone 024-018-D14 5-PRIME, mRNA sequence.
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Pred. No. 2.6e+02;
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/db_xref="taxon:161934"
/clone="024-018-D14"
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Taeniopygia guttata
Taeniopygia guttata
Taeniopygia guttata
Taeniopygia guttata
Archosauria: Aves; Neognathae; Passeriformes; Estrildidae;
Estrildinae; Taeniopygia.
Estrildinae; Taeniopygia.
Estrildinae; Taeniopygia.
Clayton, D.F., Arnold, A.P., Ball, G.F., Brenowitz, E., George, J.M., Mello, C.V., Wade, J., Replogle, K., Lewin, H., Band, M., Hernandez, A. and Liu, L.
The Songbird Neurogenomics Initiative: An Evolving Public Resource for Study of Genes, Brain, and Behavior
Contact: David F. Clayton
University of Illinois
Bl07 CLSL, 601 S. Goodwin, Urbana, IL 61801, USA
Tel: 217 244 1648
Email: dclayton@wiuc.edu
Base Calling/Quality Scores: PHRED from Washington University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage_slate_mbryo, post-hatch days 1, 10, 20, 45, and adult (pooled)"
/lab_host="DH10B"
/clobe_lib="normalized Keck-Tagu Library SB02"
/clobe_lib="normalized Keck-Tagu Library SB02"
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/note="Organ: brain; Vector: pBS II SK(+); Site_l:
ECORI(5' side_of insert); Site_2: NotI (3' side_of insert); The library was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research (6): 791-806. An identiying tag was added at the 3'during cDNA synthesis:
insertAAAAAAAAAAAAAAAAAGCGA."
                                                            SB02015B1H11.fl normalized Keck-Tagu Library SB02 Taeniopygia guttata cDNA clone SB02015B1H11.fl 5, mRNA sequence. CK302404 GK302404.1 GI:44811978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center PHRAP suite. Low quality bases (Phred score < 20) were trimmed from both ends of the sequence by an in-house script. This sequence is vector free and at least 200 bp in length. Funded by PHS grant # RO1 NSO45264, 'Songbird Neurogenomics Initiative.'
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Vector Trimming: Cross_match from Washington University Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. .752
/organism="Taeniopygia guttata"
/org.be="mRNA"
/db_xref="taxon:59729"
/clone="SB02015B1H11.f1"
/tissue_type="brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FORWARD: TAATACGACTCACTATAGGG (T7)
BACKWARD: ATTAACCCTCACTAAAG (T3)
Insert Length: 752 Std Brror: 0.00
Plate: SB02015B1 row: H column: 11
Seq primer: TAATACGACTCACTATAGGG (T7)
High quality sequence stop: 752.
Location/Qualifiers
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source

FEATURES

Matches

ORIGIN

RESULT 3 BQ590872

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Gaps : 0

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High quality sequence stop: 614.
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KEYWORDS
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CN781966
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwalp4 (gel #4732114 [gb] AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and punified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli Xii0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A79 bp DNA linear GSS 18-NOV-2003
ZMMBBD0351K10.r ZMMBBb Zea mays genomic clone ZMMBBb0351K10 3',
Genomic survey sequence.
CG853284
GC853284.1 GI:38380145
GSS.
                                                                                                                                                                                                                                                                              Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 330)
Dunn, D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mammoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
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Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab host="E. Coli strain XL10-Gold, T1-resistant, F-" /clone lib="Mouse lokb plasmid UGCIM library" /note="Wector: PWD42nv; Purified genomic DNA from Musculus C57BL/64 (male) was obtained from the Jackson Laboratory Mouse DNA Resource
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                                                                                                                                                                                                                                                                                                                                                                         Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0152 row: F column: 11
Seg primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Mus musculus"
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:10090"
/clone="UUGC2M0152F11"
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                                                                                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
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Best Local Similarity
Matches 21; Conserv
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CG853284/c
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AUTHORS
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1. (Dasses 1 to 479)

2. Yu, Y., Kim, H.R., Hatfield, J., Soderlund, C., Bharti, A.K., Messing, J. and Wing, R.

Sequencing of the maize genome

1. Unpublished (2003)

2. Contact: Rod Wing

Arizona Genomics Institute
Unpublished (2003)

Contact: Rod Wing

Arizona Genomics Institute
University of Arizona

Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ

85721-0088, USA

Tel: 520 628 3967

Fax: 520 621 9288

Email: http://genome.arizona.edu
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Chenopodium quinoa
Chenopodium quinoa
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Bukaryota, Magnoliophyta; eudicotyledons, core eudicots,
Caryophyllales; Amaranthaceae, Chenopodium.
1 (basea I to 614)
1 (basea I to 614)
Coleman, C.E., Maughan, P.J., Stevens, M.R., Jellen, E.N. and
Fairbanks, D.J.
Single nucleotide polymorphism discovery using quinoa expressed
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/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Zea mays L. ssp. mays"
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Other ESTS: EST00098
Other ESTS: EST00098
Condict: Coleman, Craig E.
Condern of Plant and Animal Sciences
Brigham Young University
275 WIDB, Brigham Young University, Provo, UT 84602, USA
725: (801) 422-5145
Fax: (801) 422-5145
Fax: (801) 422-0008
Email: craig_coleman@byu.edu
Plate: 01 row: C column: 13
Seq primer: M13 Forward
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/cultivar="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BACKWARD: M13r
Plate: 0351 row: K column: 10
SGq primer: M13r
Class: BAC ends.
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/clone="ZMMBBb0351K10"
/lab_host="DH10B"
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/organism="Zea mays"
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CN781966.1 GI:47561430
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/clone_lib="WGGS-ZmaysF (DH5a methyl filtered)"
/note="Organ: immature ears: Site_1: Xba I; Site_2: Xba I;
/note="Organ: immature ears: Site_1: Xba I; Site_2: Xba I;
revector was digested with Xba I and one nuclecitie was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between O.8 and 3 kb and were cloned into the vector (:x/y
reads in Mi3mpl9; .b/g reads in pUCl9). The same ligation
was transformed into DH5a."
                                                                                                                                                                                                                                                                                                                                          BZ618666 655 bp DNA linear GSS 16-JAN-2003 ig32b07.bl WGS-ZmaysF (DH5a methyl filtered) Zea mays genomic clone ig32b07.5', genomic survey sequence.
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Mukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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S Rabinowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N., Ratzenburger, P., King, L., Miller, B., Muller, S., Nascimento, L., Zutavern, T., McCombie, W.R., and Martienssen, R.A. Genomic shotgun sequences from Zea mays (methyl-filtered) Unpublished (2002)

Contact: W. Richard McCombie Lita Annenberg Hazen Genome Sequencing Center Cold Spring Hazen Genome Sequencing Center Cold Spring Hazen Genome Sequencing Tel: 516 367 8844

Fax: 516 367 8874

Email: mccombie@cehl.org
sites. The ligation products were transformed i electrocompetent cells (BRL Life Technologies).
                                                                                                                                            Gaps
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                                                                                           Length 626;
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                                                                                        Score 18.6; DB 8;
Pred. No. 4.9e+02;
0; Mismatches 4
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tive 0; Mismatches 4
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Seg primer: -21M13UnivFwd
Class: shotgun
High quality sequence stop: 655.
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/cultivar="B73"
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/organism="Zea mays"
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                                                                                             74.4%;
84.0%;
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  ECORI
DH10B
                                                                                                                   Similarity
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CN782003
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                                                                                                                                                                                                                                                                                                               RESULT 8
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Bukaryora, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryora; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 626)

Salao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S.,

Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de
Jong, P. and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-23

Unpublished (1999)

Other GSSs: RPCI-23-28P12.TV

Contact: Shaying Zhao

Department of Eukaryoric Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200

Fax: 301 838 0200

Fax: 301 838 0200

Email: szhao@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)

or from Resea of Genetics (info@resgen.com). BAC end page:

http://www.ligr.org/tdb/bac_ends/mouse/bac_end_intro.html

Plate: 28 row: P column: 12
Seq primer: 28 row: P column: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          626 bp DNA linear GSS 12-MAY-2000 RPCI-23-28P12, genomic clone RPCI-23-28P12, population curvey sequence.
                                                                                                                                                                                                                                       /note="Organ: Flowers; Vector: pTriplEx2; Site 1: Sfil; Site_2: Sfil; Floral cDNA Library from Chenopodium quinoa"
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/lab host="DH10B"
/clone_lib="RPCI-23"
/note="Organ: Kidney/Brain, Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Pemale C57BL/6J mouse kidney_and/or
Brain genomic DNA was isolated and partially digested
with a combination of ECORI and ECORI Methylase.
selected DNA was cloned into the pBACe3.6 vector at the
                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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74.4%; Score 18.6; DB 7; Length 614;
Best Local Similarity 84.0%; Pred. No. 4.9e+02;
Matches 21; Conservative 0; Mismatches 4; Indels

    .614
    organism="Chenopodium quinoa"

                                                                     /mol type="mRNA"
/cultivar="Real"
/db xref="taxon:63459"
/clone="F01C13"
/dev stage="pre-anthesis"
/lab host="XL-1 Blue"
/clone_lib="cqfloral"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/strain="C57BL/6J"
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clone="RPCI-23-28P12"
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Gaps

us-10-808-187a-2475.rst

VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

JOURNAL

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TITLE

FEATURES

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CG116875 945 bp DNA linear GSS 20-AUG-2003 PUKBP30TB ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0782E12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 945)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Besnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
                                                                                                                                                                                                                                                        /db_xrefe"taxon:4577"
/clone="zmMBTa0786015"
/clone_lii="zm_06_1.0 KB"
/note="Vector: pCR4-TOPO, Site_1: EcoRI; 0.6-1.0 kb high
COT selected genomic DNA library"
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Strain="B173"
/db xref="taxon:4577"
/clone="ZNMBTa0782E12"
/cone lib="ZM 0.6 1.0 KB"
/note="Vector: PCR4-TOP0; Site_1: ECOR1; 0.6-1.0 kb high
COT selected genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 842,
9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843
Far: 301-838-5843
Fars: 301-838-50208
Fars: whitelaw@rigr.org
Seq primer: TF
Class: sheared ends.
Location/Qualifiers
1...842
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                                                                                                                                                                                                              /mol_type="genomic DNA"
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                                                                                                                                                                                           /organism="Zea mays"
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Location/Qualifiers
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Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: whitelaw@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Other GSSs: PUKBP30TD
Contact: Cathy Whitelaw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GI:34000312
                                                                                                                                                                                                                                       /strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 301-838-5843
Fax: 301-838-0208
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  CN782003 672 bp mRNA linear EST 21-MAY-2004 EST00098 cgseed Chenopodium quinoa cDNA clone S01A15 5' similar to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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                                                                                                                                                         Chenopodium quinoa transcripture, Embryophyta; Embryophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllales; Amaranthaceae; Chenopodium.

1 (bases 1 to 672)

2 (coleman, C. E., Maughan, P. J., Stevens, M.R., Jellen, E. N. and Fairbanks, D. J.

Single nucleotide polymorphism discovery using quinoa expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 842)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and Bennetzen, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone lib="cgseed" / clone lib="cgseed" / clone="Vector: pTriplEx2; Site_1: Sfil; Site_2: Sfil; Developing Seed cDNA Library from Chenopodium quinoa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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PUKCM44TD ZM_0.6_1.0_KB Zea mays genomic clone ZMMBTa0788G15,
                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2004)
Other ESTs: EST00061
Contact: Coleman, Craig E.
Department of Plant and Animal Sciences
Brigham Young University
275 WIDB, Brigham Young University
Fal: (801) 422-5145
Pax: (801) 422-0008
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/organism="Chenopodium quinoa"
/mol type="mRNA"
/cultivar="Real"
/db xref="teaxon:63459"
/clone="S01A15"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="Developing Seed"
/lab host="XL-1 Blue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: craig_coleman@byu.edu
Plate: 01 row: A column: 15
Seq primer: M13 Forward
High quality sequence stop: 672.
Location/Qualifiers
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                                                                                                                                          Chenopodium quinoa (quinoa)
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CG137686
CG137686.1 GI:34028361
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Other GSSs: PUKCM44TB
Contact: Cathy Whitelaw
                                                                                          CN782003.1 GI:47561467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 84.03
Les 21; Conservative
                                                                                                                                                                                                                                                                                                                                                       sequence tags
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KEYWORDS SOURCE ORGANISM

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VERSION

TITLE JOURNAL COMMENT

REFERENCE AUTHORS

CG137686/c DEFINITION

RESULT 10

Best Loc Matches

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ORIGIN

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Imboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared bNA
was blunt end-repaired with T4 DNA polymerase and T4
polymucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, 84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="B. coli strain XL10-Gold, T1-resistant, F-" /clone_lib="Mouse_lokb plasmid UGGC9M library" /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (female) was obtained from the Jacks
l (bases 1 to 728)

Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunmgenetics.utah.edu
Commert.ength: 10000 Std Error: 0.00
Plate: 0287 row: F column: 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .728
/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: CGTTGTAAAACGACGGCCAGT
                                                                                                                                                                                                 Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC2M0287F19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 728
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AW275602/c
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                                                                                                                        607 bp mRNA linear EST 03-MAY-2004 tae17c11.y1 Hydra EST Darmsradt I Hydra magnipapillata cDNA 5' similar to SW:FUMH HUMAN P07954 FUMARATE HYDRATASE, MITOCHONDRIAL PRECURSOR;, mRNA Sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                    Hydridae; Hydra.

1 (bases 1 to 607)

Bode, H., Blumberg, B., Steele, R., Wigge, P., Gee, L., Nguyen, Q.,

Martinez, D., Kibler, D., Hampson, S., Clifton, S., Pape, D., Marra, M.,

Mallier, L., Martin, J., Wylie, T., Dante, M., Theising, B., Bowers, Y.,

Gibbons, M., Ritter, E., Bennett, J., Ronko, I., Tsagareishvili, R.,

Maguire, L., Kennedy, S., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ999859 17-APR-200 2M028719F Mouse 10kb plasmid UUGC2M library Mus musculus genomic clone UUGC2M0287F19 F, genomic survey sequence.
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Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Library was constructed by Corina Guder / GATC Konstanz, Germany Library materials provided by Thomas Holstein / Molecular Cell Biology, TUD. Darmstadt DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Hans Bode (hrbode@uci.edu)
                                                                                                                                                                                                                                                                                                                                       Hydra magnipapillata
Hydra magnipapillata
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
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WashU Hydra EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
FTE1: 314 286 1800
Fax: 314 286 1810
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/clone lib="Hydra EST Darmstadt I"
/note="Wetcor: pBluescript II SK (+); Site_1: NotI;
Site_2: EcoRI"
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/lab_host="TransforMax EC100 (Epicentre), Tl Phage
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/mol_type="mRNA"
/strain="sf-1 mutant of strain 105"
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Pest Local Similarity 90.5%; Pred. No. 6.1e+02;
Matches 19; Conservative 0; Mismatches 2;
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Location/Qualifiers
                        454 GCTATGAACCTAGACACACATTAT 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   433 TGAACCANGAAGCAGTATTAT 453
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GSS.
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Other_ESTs: tae17c11.x1
                                                                                                                                                                                                                                                                                      CN552254.1 GI:46961558
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                                                                                                           Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Produrement: John F. Bnsley, M.D., Silvio Gutkind Ph.D.,
Tissue Produrement: John F. Bnsley, M.D., Silvio Gutkind Ph.D.,
Chidchanok Leethanakul D.D.S., Michael Emmert-Buck M.D. Ph.D.
CDNA Library Preparation: David B. Krizman, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NOT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llhi.gov/Dbpy/mage/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 186.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib=_NCI_CGAP_HN11"
/note="Organ: tongue; Vector: pAMP10; cDNA made by
oligo-dr priming. Non-directionally cloned into the UDG
slites of pAMP10. Size-selected on agarose gel, average
insert size 500 bp. Primary library; non-amplified.
Reference: Krizman et al. (1996) Cancer Research
56:5380-5383."
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1 (bases 1 to 289)
Auffray, C., Behar, G., Bois, F., Bouchier, C., da Silva, C., Devignes, M.D., Duprat, S., Houlgatte, R., Jumeau, M.N., Lamy, B., Sebastiani-Kabaktchis, C. and Tessier, A. Pietu, G., Pouliot, Y., Sebastiani-Kabaktchis, C. and Tessier, A.
1 (bases 1 to 187)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Genethon Centre de recherche sur le Genome Humain
1,rue de l'Internationale, BP60 91002 EVRY Cedex, FRANCE
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95277534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72.8%; Score 18.2; DB 2; Length 187; 83.3%; Pred. No. 6.9e+02; tive 0; Mismatches 4; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /olone="IMAGE:2742603"
/tissue_type="normal squamous epithelium"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Fax: 33160778698
Email: genexpress@genethon.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
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Z45641.1 GI:574873
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Matches 20, Conservative
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                                                                             Tumor Gene Index
Unpublished (1997
                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .187
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Z45641/c
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/clone_forgan: brain; Vector: lafmid BA; Site_1: HindIII;
Site_2: NotI; sex=Female; dev_stage=3 months_old;
lsolate=muscular atrophy patient; tissue_type=total
brain; total mRNA was oligo-(dT) primed and directionally
cloned 5' -> 3' into the HindIII -> NotI sites of the
lafmid BA vector. Clone library from B.Soares, Psychiatry
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Single read.
Genexpress_library_idt: C; Genexpress_sequence_idt: y1c-zqd03
Seq_primer: (-21)M13_universal.
Location/Qualifiers
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Pred. No. 7.1e+02;
0; Mismatches 3;
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                                                                                                                  /organism="Homo sapiens"
                                                                                                                                                            /db_xref="taxon:9606"
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                                                                                                                                       /mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72.8%;
                                                                                                                                                                                                         /sex="Female
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20; Conservative
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Matches 20; Conservat
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14

16 100.0 29350 14 AY395001 AY395001 SARS 16 100.0 29350 14 AY395002 AY395002 SARS 16 100.0 29530 14 AY394985 AY394985 AY394985 SARS 16 100.0 29533 14 AY394985 AY394985 AY394985 SARS 100.0 29553 14 AY394985 AY3985 AY3	25 16 100.0 29573 14 AY338175 AY338175 SARS COFO 26 16 100.0 29577 14 AY548314 AX559094 AX559094 SARS COFO 27 16 100.0 29592 14 AY53059 AX559094 SARS COFO 28 16 100.0 29592 14 AY53059 AX559094 SARS COFO 29 16 100.0 29620 14 AY395004 AY395004 SARS COFO	16 100.0 29640 14 AY394978 AY394978 AY394979 SARS 16 100.0 29645 14 AY394982 AY394979 AY394979 AY394979 SARS 16 100.0 29647 14 AY395003 AY3950003 AY3950003 AY3950003 AY395003 AY395003 AY395003 AY395003 AY3950003 AY3	16 100.0 29665 14 AY394988 AY394988 16 100.0 29670 14 AY595982 AY594988 15 100.0 29670 14 AY559082	16 100.0 29689 14 AY394983 AX394983 SARS 16 100.0 29689 14 AY394983 AX394983 SARS	16 100.0 29705 14 AY283795 AY283795 16 100.0 29705 14 AY394980 AY394980 16 100.0 29706 14 AY283797 AY283797	16 100.0 29709 14 AY394987 16 100.0 29710 14 AY559091 16 100.0 29711 14 AY283794	ALIGNMENTS	RESULT 1 AY307165 LOCUS AY307165 1269 bp RNA linear VRL 09-JUN-2003 DEFINITION SARS coronavirus nucleocapsid protein (NP) gene, complete cds. ACCESSION AY307165	SOURCE SARS coronavirus ORGANISM SARS coronavirus Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.	REFERENCE 1 (bases 1 to 1269) AUTHORS Sun,K., Anwar,A., Gupta,V., Tabiin,M.T., Atkinson,R., Chandrasekarn,A. and Aucust.T.J.	TITLE Direct Submission JOURNAL Submitted (26-MAY-2003) Genetic Immunotherapy Lab, Johns Hopkins Singapore, 41 Science Park Road, #03-18 The Gemini, Singapore,	FEATURES Location/Qualifiers	ı	/mol_type="genomic kNA" /db_xref="taxon:227859" gene 1.1269 /mana="ND"	CDS 1, 1269 /gene="NP"	/note="associated with virus genomic kNA; involved in Cil response" /codon_start=1	/product="nucleocapsid protein" /protein id="AAP49024.1" /db_xref="GI:31540949"	/translation="MSNNGPQSNQRSARKITFGGFIDSTDNNGNGKNGKREPY GLIDSTDNNGNGKNGKREPY GLIDSTDNNGNGKNGKNGKREPY GLIDSTDNNGNGKNGKNGKNGKNGKNGKNGKNGKNGKNGKNGKNGKN	QLPQGTTLPRGSRGSQQSSRSSRSNSRNSTRNSTRNSTRNSTRSSSRGNSFRRG ALALLLLDRLNQLESKVSGKGQQQQQTVTKKSAAEASKKPRQKTTATKQYNVTQAFG RRQPEQTQGNFGDQDLIRQGTVXKHPQTAGAPSASAFFGMSRIGMEVTPSGTWLTY HGA YKI, DDRFNNYTI, JRHT I DA YKTFDPTFBKTKKKTNFRQDF, POROKKOR	TILLPADMDDFSRQLQNSMSGASADSTQA"
GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.	OM nucleic - nucleic search, using sw model Run on: May 15, 2005, 21:16:45 ; Search time 382.5 Seconds (without alignments) 2026.885 Million cell updates/sec	Title: US-10-808-187A-2476 Perfect score: 16 Sequence: 1 accccaaggtttaccc 16	Scoring table: IDENTITY NUC Gapop 10.0 , Gapext 1.0	hed: 47082	umbër od DB seq	sed length: ssing: Minimu Maximu Listir	enEmbl:*	1: gb_ba:* 2: gb_htg:* 3: gb_in:* 4: gb_om:* 6: gb_ow:*	8 g g g		Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	Result Query No. Score Match Length DB ID Description	16 100.0 1269 14 AY307165 AY307165 SARS 160.0 1269 14 AY360146 AY360146 SARS 16 100.0 1269 14 AY360146 AY360146 AY360146 AY360146 AY360146 AY360146 AY360146 AY360146 AY360146 AY360136	16 100.0 1669 14 AY536760 AY536760 SARS 100.0 1873 14 AY53475854 AY534761 SARS	16 100.0 1938 14 AY534762S6 AY514767 SARS 16 100.0 2304 14 AY322205S4 AY322205SARS 16 100.0 2810 14 AY290752 AY290752 SARS	16 100.0 3080 14 AY43086S10 AY443095 SARS 16 100.0 8439 14 AY304489 AY304489 SARS 16 100.0 8581 14 AY304487 AY304487 SARS	2 16 100.0 11006 14 AY304491 AY304491 SARS 3 16 100.0 11010 14 AY304493 AY304493 SARS 4 16 100.0 11010 14 AY304494 AY304494 SARS	AY304490 AY304492 AY463060 AY300000	16 100.0 29350 14 AI395000 AY395000 SARS

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/gene="NP"
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REPERQTGGORFEDODLIRGYTDYKHWPDIAOPAPSASAFFGMSRIGMEVTPSGTWLTY
HGAIKLDDKDPPRONVILLANKHIDAYKTFPPTEPKKDKKKKTDEAQPLPQRQKKQPT
VTLLPAADMDDFSRQLQNSMSGASADSIQA"
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1 (bases I to 1269)

Zhu,H.P., Lu,Q.Y., Lu,Y.Y., Yao,P.P., Xu,F., Ge,Q., Weng,J.Q., Yan,J.Y., Gong,L.M., Shi,W., Zhao,Z.Y. and Zhu,Z.Y.
Cloning and expression of nucleocapsid protein gene of SARS associated coronavirus
                                                                                                                                                                                                                                AY360146 1269 bp RNA linear VRL 02-SEP-2003 SARS coronavirus HPZ-2003 nucleocapsid protein (NP) gene, complete
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Zhu,H.P., Lu,Q.Y., Lu,Y.Y., Yao,P.P., Xu,F., Ge,Q., Weng,J.Q.,
Xan,J.Y., Gong,L.M., Shi,W., Zhao,Z.Y. and Zhu,Z.Y.
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                                   Score 16; DB 14; Length 1269;
Pred. No. 3e+02;
Mismatches 0; Indels 0
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SARS coronavirus HPZ-2003
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                                 Query Match
Best Local Similarity 100.0%;
Matches 16; Conservative 0
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/gene="NP"
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Matches 16; Conservative
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QLPQCTTLPKGFYAEGSRGGSQASSRSSRRGRGNSRNSTPGSSRGNSPARMASGGGET
ALALLIDRLNRLESKVSGKGQQQGQTVTKKSAABASKKPRQKRTATKQYNVTQAFG
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KELSPRWYFYYLGTGPEASLPYGANKEGIVWVATEGALNTPKDHIGTRNPNNNAATVL
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SARS coronavirus BJ01 nucleocapsid protein mRNA, complete cds.
AYS57760
AY536760.3 GI:52100973
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.

1 (bases 1 to 1269)
Timani, K.A., Ye,L., Ye,L., Zhu,Y., Wu,Z. and Gong,Z. Cloning, sequencing, expression, and purification of SARS-associated coronavirus nucleocapsid protein for serodiagnosis
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Coronaviridae; Coronavirus.

Li, T, and Liu, L.

Identification of SARS-COV mRNA leader sequence
Unpublished
                                                                                                                                                                                                                                                                                                                   Timani,K.A., Ye,L., Ye,L., Zhu,Y. and Guo,D.
Direct Submission
Submitted (11-400-2003) Institute of Virology, Wuhan University,
Wuhan, Hubei 43072, P.R. China
Location/Qualifiers
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Li.T., Li.X., Liu.L. and Chang, Z.
Direct Submission
Submitted (30-JAN-2004) Institute of Biomedicine, Tsinghua
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                                                                                                                                                                                                                                                                                                                                                                                                         /product="nucleocapsid protein"
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KELSPRWYFYXLGTGPEASLPYGANKEGIVWVATEGALNTPKDHIGTRNPNNNAATTU
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Submitted (28-JAN-2004) Genome Institute of Singapore, 60, Biopolis
Street, 02-01, Genome, Singapore 138672, Singapore
Location/Qualifiers
1. .1873
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KREPEQTQGRGDQDLIRQTDYKHPDLAQPAPSASAFFGNSRIGMBYTPSGTWLTY
KGA KLDDKDPQFKNVTLLANKTIDAYKTFPPTBPKKDKKKTDEAQPLPQRQKKQPT
VTPLPAADMDDFSRQLONSMSGASADSTQA"
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SARS coronavirus Sin0409
SARS coronavirus Sin0409
SARS coronavirus Sin0409
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.

1 (bases 1 to 1873)
Viruses; Kurup, A., Gopalakrishna, G., Chan, K.P., Wong, C.W.,
Ng, L.C., Se-Thoe, S.Y., Oon, L., Bai, X., Stanton, L.W., Ruan, Y.,
Miller, L.D., Vega, V.B., James, L., Ooi, P.L., Kai, C.S., Olsen, S.J.,
Ang, B. and Leo, Y.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 1873)
Wei,C.L., Lee,C., Lin,S., Thoreau,H., Vega,V.B., Stanton,L.W. and
University, Beijing, Beijing 100084, China

Sa (bases 1 to 1669)

Li,T., Li,X., Liu,L. and Chang,Z.

Direct Submission

Submitted (06-JUL-2004) Institute of Biomedicine, Tsinghua University, Beijing, Beijing 100084, China
Sequence update by submitter

4 (bases 1 to 1669)

Li,T., Li,X., Chang,Z. and Liu,L.

Direct Submission

Submitted (15-SEP-2004) Institute of Biomedicine, Tsinghua University, Beijing 100084, China
Sequence update by submitter
On Sep 15, 2004 this sequence version replaced gi:49921010.
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SARS coronavirus Sin0409, partial sequence.
AY534761
                                                                                                                                                                                                                                                                                    organism="SARS coronavirus BJ01"
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Pred. No. 2.9e+02;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/strain="BJ01"
/db_xref="taxon:228407"
                                                                                                                                                                                                                                                                                                                                                       country="China"
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                                                                                                                                                                                                                                                                                                                                                                                          codon_start=1
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1 Similarity 100.0%;
16; Conservative 0;
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Best Local Similarity
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(Dassel 1 to 19.4).

Lim, P.L., Kurub, A., Gopalakrishna, G., Chan, K.P., Wong, C.W., Ng, L.C., Se-Thoe, S.Y., Oon, L., Bai, X., Stanton, L.W., Ruan, Y., Miller, L.D., Vega, V.B., James, L., Ooi, P.L., Kai, C.S., Olsen, S.J., Ang, B. and Leo, Y.S.

Laboratory-acquired severe acute respiratory syndrome (SARS) - Singapore 2003
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Wei,C.L., Lee,C., Lin,S., Thoreau,H., Vega,V.B., Stanton,L.W. and
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1 (bases 1 to 2304)
Yuan, Z., Zhang, X., Hu, Y., Lan, S., Wang, H., Zhou, Z. and Wen, Y.
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Submitted (28-JAN-2004) Genome Institute of Singapor
Street, 02-01, Genome, Singapore 138672, Singapore
Location/Qualifiers
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/db_xref="taxon:26647"
/country="Singapore"
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/db_xref="taxon:266148"
/country="Singapore"
                                                                                                                                                                                                                                                                                                                                                                                                                    AYS34762S6 1938 bp RNA SARS coronavirus Sin_WNV, partial sequence. AYS34767
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                                                                                                                                            100.0%; Score 16; DB 14; 100.0%; Pred. No. 2.9e+02;
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SARS coronavirus Sin_WNV
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Submitted (05-DEC-2003) Department of Microbiology, Zhejiang Center of Disease Prevention and Control, 17 Laozheda Rd., Hangzhou, Zhejiang 310009, China Nucleotide and amino acid sequences updated by submitter on Dec 5, 2003 this sequence version replaced gi:31505969.
                                                                                                                                                                                                                                                                                                                                    Wang, Z.G., Li,L.J., Luo,Y., Zhang,J.Y., Wang,M.Y., Cheng,S.Y., Zhang,Y.J., Wang,X.M., Lu,Y.Y., Wu,N.P., Mei,L.L. and Wang,Z.X. Molecular biological analysis of genotyping and phylogeny of severe acute respiratory syndrome associated coronavirus Chin. Med. J. 117 (1), 42-48 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="uncharacterized protein 6"
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PFHPLADNKFALTCTSTHFAFACADGTRHTYQLRARSVSPKLFIRQEEVQQELYSPLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of Microbiology, Zhejiang Center
17 Laozheda Rd., Hangzhou,
                     Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales; Coronaviridae; Coronavirus.

1 (bases I to 2810)

Li,Li, Wang, Z., Lu, Y., Bao, Q., Chen, S., Wu, N., Cheng, S., Weng, J., Zhang, Y., Yan, J., Mei, L., Wang, X., Zhu, H., Yu, Y., Zhang, M., Li, M., Yao, J., Lu, Q., Yao, P., Bo, X., Wo, J., Wang, S. and Hu, S. Severe acute respiratory syndrome-associated coronavirus genotype and its characterization

Chin. Med. J. 116 (9), 1288-1292 (2003)
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/note="transcription regulatory core sequence
867. .986
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/note="transcription regulatory core sequence
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/protein_id="AAR27475.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J (bases 1 to 2810)
Wang,Z., Cheng,S., Zhang,Y., Lu,Y. and Mei,L.
Direct Submission
Direct (31-MX-2003) Department of Microbic of Disease Prevention and Control, 17 Laozhedë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhejiang 310009, China
4 (bases 1 to 2810)
Wang,Z., Cheng,S., Zhang,Y., Lu,Y. and Mei,L.
Direct Submission
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/mol type="genomic RNA"
/isolate="ZJ01b"
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/country="China: Hangzhou"
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KELSPRWYFYLGTGPEASLPYGANKEGIVWATGBALNTPKCHIGTRNPNNNATVL
OLPQGTTLPKGFYAEGSRGGSQASSRSSRSRGNSRNSTPGSSRRGNSPARMASGGGET
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KREPEQTGGRGDQDLTRQCTDYKHWDQLAQFARSASAFRGMSRIGMEAAPSGTWLTY
HGAIKLDDKUPQFKDNVILLIAKHIDAYKTFPPTEPKKDKKKTDEAQPLPQRQKKQPT
VTLLPAADMDDFSRQLQNSMSGASADSTQA
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Direct Submission
Submitted (12-JUN-2003) Molecular Virology, Shanghai Medical
College of Fudan University, 138 Yi Xue Yuan Road, Shanghai 200032,
P.R. China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="Orf8A"
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    .2304
    /organism="SARS coronavirus Shanhgai LY"

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/country="China: Shanghai"
                                                                                                              Location/Qualifiers
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                                                                                                                                                                                                                                                                     <1. .276
/codon start=1
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KDLPKEITVATSRTLSYYKLGASQRVGTDSGFAAYNRYRIGNYKLNTDHAGSNDNIAL
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                                                                 Chim, S.S.C., Tong, Y.K., Hung, E.C., Chiu, R.W. and Lo, Y.M. Direct Submission
Submitted (20-OCT-2003) Chemical Pathology, Chinese University of Hong Kong, Prince of Wales Hospital, 30-32 Ngan Shing Street,
                                                                                                                                                                                                                                      organism="SARS coronavirus CUHK-L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
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Clin. Chem. 50 (1), 231-233 (2004) 14709660
                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAS01066.1"
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                                                                                                                                                           Shatin, Hong Kong, China
Location/Qualifiers
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| Da xref="G1:31747888"
| Cranslation="MEMOTIVPDPALHLVDPQIOLTITRMEDAMGGGQNSADPKVYP
| ILIRLGSQLSLSMARRNLDSLEARAFQSTPIVVQMTKLATTEELPDEFVVVTAK"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALALLLLDRINQLESKVSGKGQQQGGTVTKKSAAEASKKPRQKRTATKQYNVTQAFG
KROPBQTQGSNGBQDLIRQSTDYKMPOLAQPAPSASAFFGMSRIGMBYTPSGTWLTY
KGAIKLDDKOPQFKNVTILINKHIDAYKTFPPTEPKKDKKKKTDEAQPLPQRQKKQPT
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                                                                                                                                                                                                                                                                               /trānslation="MCLKILVRYNTRGNTYSTAWLCALGKVLPFHRWHTMVQTCTPNV
TINCQDPAGGALIARCWYLHEGHQTAAFRDVLVVLNKRTN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /trānslation="MSDNGPQSNQRSAPRITFGGPTDSTDNNQNGGRNGARPKQRRPQ
GLPNNTASWFTALTQHGKEELRFPRGQGVPINTNSGPDDQIGYYRRATRRVRGGDGKM
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QLPQGTTLPKGFYAEGSRGGSQASSRSSSRSRGNSRNSTPGSSRGNSPARMASGGGET
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1 (bases 1 to 3080)

Chim,S.S.C., Tongy.Y.K., Hung,E.C.W., Chiu,R.W.K. and Lo,Y.M.D.
Genomic Sequencing of a SARS Coronavirus Isolate That Predated the Metropole Hotel Case Cluster in Hong Kong
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AX443095. GI:41352885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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/note="transcription regulatory core sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   product="uncharacterized protein 9c"
                                                                                                                                          'note="Xiaohong genotype locus 7"
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Codon start=1

product="nucleocapsid protein"

protein id="AAP44772.1"

db_xref="GI:31505970"
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'db_xref="GI:38735514"
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SARS coronavirus CUHK-L2
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                                                                                                                                                                                                                                                                           SARS coronavirus SZ13
SARS coronavirus SZ13
Viruses; ssRNA positive strand viruses, no DNA stage; Nidovirales;
Coronavirus Coronavirus.
1 (bases 1 to 8581)
Guan, Y., Zheng, B.J., He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L.,
Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L.,
Poon, L.L.M.
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SARS coronavirus GZ60
SARS coronavirus GZ60
SARS coronavirus GZ60
Coronaviridae, Coronavirus.

1 (bases 1 to 11006)
GGuan, Y., Zheng, B.J., He, Y.O., Liu, X.L., Zhuang, Z.X., Cheung, C.L., Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L., Chan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and Poon, L.L.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (26-MAY-2003) Microbiology, The University of Hong Kong,
University Pathology Building, Queen Mary Hospital, Pokfulam Road,
                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolation and characterization of viruses related to the SARS coronavirus from animals in southern China Science 302 (5643), 276-278 (2003)
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/mol type="genomic RNA"
isolate="SZ13"
/db_xref="taxon:231514"
/country="Hong Kong"
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100.0%; Pred. No. 2.5e+02;
iive 0; Mismatches 0;
             Pred. No. 2.5e+02;
Mismatches 0;
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                                                                                                                                                                                       SARS coronavirus SZ13, partial genome. AY304487
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100.08;
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AY304491.1 GI:34482142
                                                                                         7115 ACCCAAGGTTTACCC 7130
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Guan, Y. and Zheng, B.J.
Direct Submission
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                                                                  1 ACCCCAAGGTTTACCC
                                16; Conservative
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           Best Local Similarity
Matches 16; Conserv
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JOURNAL
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AY304491
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MEDLINE
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AY304487
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Ab xref="eq1:41352906"

/translation="WDPNOTWVPPALHLVDPQ10LTITRMEDAMGGGONSADPKVYP

IILRIGSQLSLSMARRNLDSLEARAFQSTP1VVQMTKLATTEELPDEFVVVTAK"
                                                                                                                     /trānslation="MCLKILVRYNTRGNTYSTAWLCALGKVLPPHRWHTMVQTCTPNV
TINCQDPAGGALIARCWYLHEGHQTAAFRDVLVVLNKRTN"
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Coronaviridae; Coronavirus.

(Lobase 1 to 8439)

Guan, Y., Zheng, B.J., He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L., Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L., Chan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and Boon, L.L.M.

Isolation and characterization of viruses related to the SARS coronavirus from animals in southern China

Science 302 (5643), 276-278 (2003)
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University Pathology Building, Queen Mary Hospital, Pokfulam Road,
Hong Kong, China
             'translation="MKLLIVLTCISLCSCIRTVVQRCASNKPHVLEDPCKVQH"
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/organism="SARS coronavirus S21"
/inol type="genomic RNA"
/isolate="S21"
/db xref="taxon:231516"
/country="Hong Kong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AY304489 8439 bp RNI
SARS coronavirus SZ1, partial genome.
                                                                /product="orf11"
/protein_id="AAS01073.1"
/db_xref="G1:41352904"
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                                2039. .2293
/codon_start=1
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codon start=1
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Guan, Y. and Zheng, B.J.
Direct Submission
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SARS coronavirus SZ1
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Best Local Similarity
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TITLE JOURNAL

FEATURES

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SARS coronavirus GZ43
SARS coronavirus GZ43
Viruses; ssRNA postrive-strand viruses, no DNA stage; Nidovirales;
Viruses; ssRNA postrive-strand viruses, no DNA stage; Nidovirales;
1 (bases 1 to 13471)
1 (ban, Y., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, R.M., Wong, R.L.,
Chan, K.W., Lim, W., Shortridge, K.F., Yuen, R.Y., Peiris, J.S.M. and
Poon, L.L.M.
                                                                              SARS coronavirus HKU-66078
SARS coronavirus HKU-66078
Coronavirus HKU-66078
Coronaviridae; Coronavirus.
1 (bases 1 to 11010)
Guan, Y., Zheng, B. J., He Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L., Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Mong, K.L., Chan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and Poon, L.L.M.
Isolation and characterization of viruses related to the SARS coronavirus from animals in southern China
Science 302 (5643), 276-278 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (27-MAY-2003) Microbiology, The University of Hong Kong, University Pathology Building, Queen Mary Hospital, Pokfulam Road, Hong Kong, China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 13471)
Guan, Y. and Zheng, B.J.
Direct Submission
Submitted (27-MAY-2003) Microbiology, The University of Hong Kong, University Pathology Building, Queen Mary Hospital, Pokfulam Road, Hong Kong, China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolation and characterization of viruses related to the SARS coronavirus from animals in southern China Science 302 (5643), 276-278 (2003)
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/organism="SARS coronavirus HKU-66078"
/mol_type="genomic RNA"
/isolate="HKU-66078"
/db.xref="texon:231521"
/country="Hong Kong"
    SARS coronavirus HKU-66078, partial genome.
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100.0%; Pred. No. 2.4e+02;
ive 0; Mismatches 0;
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AY304490
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1. .13471
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                          AY304494.1 GI:34482145
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2 (bases 1 to 11010)
Guan, Y. and Zheng, B.J.
Direct Submission
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Best Local Similarity 100.0%;
Matches 16; Conservative 0
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SARS coronavirus HKU-65806
Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
Coronaviridae; Coronavirus.
1 (bases 1 to 11010)
Guan, Y., Zheng, B.J., He, Y.Q., Liu, X.L., Zhuang, Z.X., Cheung, C.L.,
Luo, S.W., Li, P.H., Zhang, L.J., Guan, Y.J., Butt, K.M., Wong, K.L.,
Chan, K.W., Lim, W., Shortridge, K.F., Yuen, K.Y., Peiris, J.S.M. and
Poon, L.L.M.
Isolation and characterization of viruses related to the SARS
                    2 (bases 1 to 11006)
Guan, Y. and Zheng, B.J.
Direct Submission
Submitted (27-MAY-2003) Microbiology, The University of Hong Kong,
University Pathology Building, Queen Mary Hospital, Pokfulam Road,
Hong Kong, China
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (27-MAY-2003) Microbiology, The University of Hong Kong,
University Pathology Building, Queen Mary Hospital, Pokfulam Road,
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                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%; Score 16; DB 14; Length 11006; Best Local Similarity 100.0%; Pred. No. 2.4e+02; Matches 16; Conservative 0; Mismatches 0; Indels 0;
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1. .11010
/organism="SARS coronavirus HKU-65806"
/mol_type="genomic RNA"
/isolate="HKU-65806"
/db_xref="taxon:231520"
                                                                                                                                          11010 bp RNA
SARS coronavirus HKU-65806, partial genome.
AY304493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coronavirus from animals in southern China
Science 302 (5643), 276-278 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         9516 ACCCCAAGGTTTACCC 9531
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Guan, Y. and Zheng, B.J.
Direct Submission
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                                                                                                                                                                         source
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SOURCE
ORGANISM
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PUBMED
REFERENCE
AUTHORS
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REFERENCE AUTHORS

REFERENCE AUTHORS TITLE JOURNAL

FEATURES

ORIGIN

JOURNAL MEDLINE PUBMED

TITLE

RESULT 14 AY304494 LOCUS

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RESULT 13 AY304493

à 셤 VERSION

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Gaps

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VRL 05-NOV-2003

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0; Gaps
                                                                            Query Match 100.0%; Score 16; DB 14; Length 13471; Best Local Similarity 100.0%; Pred. No. 2.4e+02; Matches 16; Conservative 0; Mismatches 0; Indels 0;
/isolate="G243"
/db_xref="taxon:231517"
/country="Hong Kong"
                                                                                                                                            ORIGIN
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Search completed: May 16, 2005, 02:00:25 Job time: 382.5 secs

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May 15, 2005, 17:17:00 ; Search time 205.25 Seconds (without alignments) 461.466 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                         4390206 seqs, 2959870667 residues
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Maximum Match 1008
Listing first 45 summaries
                                                                   OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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geneseqn2004bs:*
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16
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                     Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Adj39000 SARS coro	Adq22117 Human sof	Aafil093 Fusarium	Abk76701 Bacillus	Adj39216 Plant cDN	Aai80700 Human pol	Adl98231 Human tum	Ach18176 Human adu	Ade59926 Rat gene	Add45738 Rat gene	Abv54268 Human pro	Acn87348 Breast ca	Aca43754 Prokaryot	Aca30490 Prokaryot	Adt45075 Bacterial	Adb58261 Toxicity-	Adb52793 Primary r	Ado43431 Lutzomyia	Ads49398 Bacterial	TOTAGE OF TOTAGE
SUMMARIES	ID	ADJ39000	ADQ22117	AAF11093	ABK76701	ADJ39216	AA180700	ADL98231	ACH18176	ADE59926	ADD45738	ABV54268	ACN87348	ACA43754	ACA30490	ADT45075	ADB58261	ADB52793	AD043431	ADS49398	AAC81907
	DB	12	12	m	9	12	4	11	0	10	10	S	11	œ	œ	13	10	10	12	13	4
	Query Match Length DB	29751	3319	199	257	311	315	446	473	504	504	509	629	663	1161	1239	1497	1497	1839	3272	6777
ob.	Query Match	100.0	93.8	90.0	90.0	90.06	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0	90.0
	Score	16	15	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4	14.4
	Result No.	п	8	ო ს	4	Ŋ	9	C 7	80	ი ი	c 10	c 11	c 12	c 13	c 14	c 15	16	17	18	19	20

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Leaduce NAM indecides Comparisting of the Partitis C virus (HCV); (4) inducing targeted RNA interference toward HCV in hepatic cells; (5) inhibiting replication of HCV; (6) a vector comparising a DNA segment encoding the RNA molecule; (7) a host cells comprising the vector of (6); (8) inhibiting replication of HCV in cells carrying HCV; (9) treating hepatitis C in a subject; (10) a modified siRNA molecule comprising a double-stranded RNA molecule of 10-30 nucleotides in length, which mediates RNA interference toward a target agent or virus and is linked to at least one receptor-binding ligand; and colecules have antiinflammatory, hepatorropic and virucide activities.

(11) inducing targeted RNA interference in a patient. The modified siRNA molecules are useful for inactivating virus in mammalian cells. The siRNAs are useful for treating hepatitis C virus, hepatitis D virus, hepatitis D virus, hepatitis E virus, Ebola virus, influenza virus, metapneumoniavirus, retrovirus, poliovirus, human papilloma virus, metapneumoniavirus or coronavirus infections. The methods of the invention can be used to correct or compensate for cellular physiological abnormalities involved in conferring susceptibility to viral infections in patients and/or alleviate symptoms of a viral infection in patients. The present sequence represents the SARS coronavirus nucleotide sequence, stranded RNA molecule of 10-30 nucleotides that inhibits replication of which is used in an example from the present invention.

Gaps Sequence 29751 BP; 8478 A; 5941 C; 6188 G; 9144 T; 0 U; 0 Other; ö 100.0%; Score 16; DB 12; Length 29751; 100.0%; Pred. No. 1.1e+02; Indels 0; 0; Mismatches 1 ACCCCAAGGTTTACCC 16 Local Similarity 100. hes 16; Conservative Query Match Matches

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28245 ACCCCAAGGTTTACCC 28260 ð

soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human; Human soft tissue sarcoma-upregulated DNA - SEQ ID 4937. ADQ22117 standard; DNA; 3319 BP (first entry) WO2004048938-A2. Homo sapiens. 26-AUG-2004 10-JUN-2004 ADQ22117;

26-NOV-2002; 2002US-0429739P. 26-NOV-2003; 2003WO-US038193

(PROT-) PROTEIN DESIGN LABS INC.

Zlotnik A; Aziz N, Ginsburg WM,

WPI; 2004-441208/41.

Early detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue

Example 2; SEQ ID NO 4937; 210pp; English.

The invention relates to a novel method for detecting soft tissue sarcoma which comprises obtaining a first soft tissue sample from an individual and a normal soft tissue sample from the same or different individual, determining the expression of a gene in both samples and comparing the

ö The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microcoganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture expression of the gene in both soft tissue samples, where a higher level of protein expression in the first soft tissue sample indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor. Multiple gene expression; filamentous fungal cell; EST; expressed sequence tag; Fusarium venenatum; Aspergillus niger; Aspergillus oryzae; Trichoderma resesi; identification; recombination; culture condition; environmental stress; spore morphogenesis; metabolic pathway engineering; catabolic pathway engineering; ss. oring differential expression of genes in filamentous fungal cell fluorescence-labeled nucleic acids isolated from the cells and a Gaps ; 0 93.8%; Score 15; DB 12; Length 3319; 100.0%; Pred. No. 3.3e+02; .ive 0; Mismatches 0; Indels (Sequence 3319 BP; 770 A; 828 C; 890 G; 820 T; 0 U; 11 Other; Clausen IG, Berka RM, Rey MW, Shuster JR, Kauppinen S, Fusarium venenatum EST SEQ ID NO:3616. substrate of expressed sequence tags. Claim 86; Page 1645; 3161pp; English. (NOVO) NOVO NORDISK BIOTECH INC. (NOVO) NOVO NORDISK AS. 3166 CCCCAAGGTTTACCC 3180 .093/c AAF11093 standard; cDNA; 199 22-MAR-2000; 2000WO-US007781. 99US-00273623. 2 CCCCAAGGITIACCC 16 13-MAR-2001 (first entry) 15; Conservative WPI; 2000-594572/56 Query Match Best Local Similarity Fusarium venenatum WO200056762-A2. 22-MAR-1999; 28-SEP-2000. Monitoring AAF11093; Matches uses AAF11093/ 88888888888 ò 셤

monitoring gene copy number variation and stability. Monitoring changes in expression of genes may be used to provide a representation of the way in which Badillus cells adapt to changes in culture conditions. extensive follow environmental stress or other physiological provocation. Extensive follow characterisation is unnecessary, when one spot on an array equals one gene or one open reading frame, since sequence information is available. This sequence represents a genomic sequence tag (GST) used in the method of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pot_sequences

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conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway enginecting. Using ESTS provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarray's based on function of the gene products to facilitate analysis of the results. AAF01478 to AAF11247 represents ESTS from Fusarium venenatum; AAF11248 to AAF11653 represents ESTS from Aspergillus niger; AAF11854 to AAF14878 represents ESTS from Aspergillus oryzas, and AAF14879 to AAF15337 represents ESTS from AAF16651 represents arease, which are all specifically claimed in the present
                                                                                                                                                                                                       Gaps
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                                                                                                                                                                           Length 199;
                                                                                                                                                                                                                                                                                                                                                                                                                       Differential gene expression, genomic sequenced tag, GST, altered culture condition; environmental stress; physiological provocation; ds.
                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                               Bacillus licheniformis genomic sequence tag (GST) #3992.
                                                                                                                                                    Sequence 199 BP; 45 A; 39 C; 44 G; 54 T; 0 U; 17 Other;
                                                                                                                                                                           Score 14.4; DB 3;
Pred. No. 5.8e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                     ABK76701 standard; DNA; 257 BP
                                                                                                                                                                           90.0%;
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                                                                                                                                                                                                                                               96 ACCCCAAGGTTTTCCC 81
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                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacillus licheniformis.
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Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                       13-AUG-2002
                                                                                                                            invention
                                                                                                                                                                                                                                                                                                                                              ABK76701;
                                                                                                                                                                                                                                                                                            RESULT 4
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Gaps

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90.0%; Score 14.4; DB 6; Length 257; 93.8%; Pred. No. 5.9e+02; ive 0; Mismatches 1; Indels (

ADJ39216 standard; cDNA; 311 BP

ADJ39216

(first entry)

06-MAY-2004

233 ACCCCAAGGTTAACCC 248

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1 ACCCCAAGGTTTACCC 16

Local Similarity 93.8 hes 15; Conservative

Matches

Query Match

Sequence 257 BP; 65 A; 33 C; 91 G; 68 T; 0 U; 0 Other;

Plant; gene; ss; transcription; plant genome augmentation; cereal; soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet; maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance; stress tolerance; salt tolerance; cold tolerance; drought tolerance; plant nutrition; apical dominance; dwarfism; early flowering; antiviral; 26-SEP-2001; 2001US-0325277P. 26-SEP-2001; 2001US-0325448P. 04-APR-2002; 2002US-0370620P. 26-SEP-2002; 2002US-00260238 BRIGGS S P. COOPER B. GLAZEBROOK J. Goff SA, Katagiri F, GOFF S A.
KATAGIRI F.
KREPS J.
PROVART N. WPI; 2004-190374/18. BUDWORTH P. MOUGHAMER T. Plant cDNA #216. US2004016025-A1. 22-JAN-2004. Budworth P, antifungal Eukaryota. BUDW/) (MOUG/) (COOP/) (GLAZ/) (PROV/) (RICK/) (ZHOT/) (KATA/) (KREP/) (GOFF/) The invention describes a method of monitoring differential expression of genes in a first Bacillus cell relative to expression of the genes in other Bacillus cells, comprising hybridising labelled nucleic acid probes isolated from Bacillus cells to a substrate containing array of Bacillus genomic sequenced tags (GST), examining the array, and determining relative gene expression by an observed hybridisation reporter signal of a spot in the array. The method is useful for measuring the expression of genes in a first Bacillus cell relative to expression of the same genes in no en or more second Bacillus cells. The method is useful for monitoring global expression of several genes from a Bacillus cell, discovering new genes, identifying possible functions of unknown open reading frames and Monitoring differential expression of several genes in first Bacillus cell relative to expression of same genes in one or more second Bacillus cells, by using substrate containing Bacillus genomic sequenced tag Claim 4; SEQ ID NO 3992; 200pp; English. (NOVO) NOVOZYMES BIOTECH INC. (NOVO) NOVOZYMES AS. 05-OCT-2001; 2001WO-US031437. 06-OCT-2000; 2000US-00680598. 27-MAR-2001; 2001US-0279526P. WPI; 2002-416684/44.

Berka R,

array

11-APR-2002

New rice promoter, useful for manipulating crop plants to alter or improve phenotypic characteristics, e.g. produce large quantities of oil or proteins, resistance to insecticides, virus or fungi, stress tolerance or high nutritional value. Glazebrook J; Moughamer T, Briggs SP, Cooper B, G tagiri F, Kreps J, Provart N, Ricke

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production of other cytokines in other cell populations.
                                                                                                                                                                                                                                                                                                       Matches
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                                                   The invention steam, panicle, rough and present and constitutive transcription of an operatively linked nucleic seeds.

Or constitutive transcription of an operatively linked nucleic acid segment. The invention also relates to a method for augmenting a plant genome and a method of identifying a gene, where its expression is plant c genome and a method of identifying a gene, where its expression is constitutive altered in the seed, leaf, stem, panicle, pollen, root or is constitutive canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley, cstom, peanut, tobacco or sugar beet, preferably maize, barley, cstom, peanut, tobacco or sugar beet, preferably maize, barley, cstomy peanut, tobacco or sugar beet, preferably maize, barley, cstomy peanut, the polymucleotides and the polypeptides they encode are useful for manipulating crop plants to alter or improve then the proteins, to incur resistance to insecticides, viruses or fungi, and to incur stress tolerance (e.g. salt, cold or drought) to ensure the plants have a high nutritional value with reduced apical dominance or dwarfism, early flowering or altered metabolic pathways. This sequence are presente a plant nucleic acid of the invention. Note: The sequence data for this clearing to the printed specification but was obtained in electronic format directly from USPTO at sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorders; archritis; inflammation; ss.
                                         plant nucleotide sequences that direct seed-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 311;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 311 BP; 57 A; 106 C; 87 G; 61 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          90.0%; Score 14.4; DB 12;
93.8%; Pred. No. 6e+02;
ive 0; Mismatches 1;
Claim 68; SEQ ID NO 216; 230pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human polynucleotide SEQ ID NO 760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA180700 standard; cDNA; 315 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu C, Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-FEB-2001; 2001WO-US004927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-FEB-2000; 2000US-00515126
18-MAY-2000; 2000US-00577409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ACCCCAAGGTTTACCC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71 ACCCCAAGGTTGACCC 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best_Local Similarity 93.8%;
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                         The invention relates to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P-PSDB; AAO00769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAI80700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity in the diagnosis and/or reatment of cancer, leukaemia, nervous system disorders arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determination of ability of TAXOL to reduce tumor growth in a patient, useful to choose appropriate therapy and assess continued effectiveness of therapy, uses measurement of expression of marker polynucleotides in
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human, tumour, taxane, TAXOL, sensitivity marker; resistance marker, ovarian tissue; cancer, gene, ss.
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                                                                                                                                                                                                                                                                          Score 14.4; DB 4; Length 315;
Pred. No. 6e+02;
0; Mismatches 1; Indels (
                                                                                                                                                                                                                                    Sequence 315 BP; 87 A; 57 C; 89 G; 82 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 45; SEQ ID NO 84; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brown JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADL98231 standard; cDNA; 446 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                     213 ACCCCAAGGITTTCCC 198
                                                                                                                                                                                                                                                                            90.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-APR-2001; 2001US-0284764P.
18-APR-2001; 2001US-0284773P.
31-MAY-2001; 2001US-0295031P.
                                                                                                                                                                                                                                                                                                                                                                        16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18-APR-2002; 2002US-00125159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human tumour marker gene #84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-NOV-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                        1 ACCCCAAGGTTTACCC
                                                                                                                                                                                                                                                                                                                              15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-898065/82
                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   useful to choose
of therapy, uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US2003166023-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                 Query Match
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markers are useful for producing probes or primers that selectively hybridise to polymucleotides (e.g. probes hybridising to mRNA molecules), useful for detecting polymucleotides in samples. e.g. ovarian tissue (especially tumour) samples. The polypeptides encoded by the markers are useful for identifying compounds that selectively bind to the polypeptides, useful to detect polypeptides in samples. This sequence represents a tumour marker gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH50811, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide sequences are also useful as hybridisation probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of for chromosome and gene mapping, in the recombinant production of for chromosome and generating antisense DNA or RNA The purified polypeptide is useful for generating antisense specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ss; sequencing by hybridisation; SBH; expressed sequence tag; EST; mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA libraries, useful chromosome and gene
                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotide sequences obtained from various cDNA libraries, as hybridization probes, as oligomers for PCR, for chromosome and gemapping, in the recombinant production of protein, or in generating
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                                                                                                                                                                                       90.0%; Score 14.4; DB 11; Length 446; 93.8%; Pred. No. 6.2e+02; ive 0; Mismatches 1; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Jones LW;
                                                                                                                                                                                                                                Indels
                                                                                                                                                     Sequence 446 BP; 102 A; 81 C; 174 G; 89 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Stache-Crain B, Dickson MC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 5388; 44pp; English.
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                                                                                                                                                                                                                                                                                                     310 ACCCCAAGGTTTCCCC 295
                                                                                                                                                                                                                                                                    16
                                                                                                                                                                                                                                                                                                                                                                                                  ACH18176 standard; cDNA; 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human adult heart cDNA #2490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-JUL-2001; 2001US-00918995
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                                                                                                                                                                                                                                                                1 ACCCCAAGGTTTACCC
                                                                                                                                                                       Query Match
Best Local Similarity 93.8%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
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STACHE-CRAIN B.
DICKSON M C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drmanac RT, Labat I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antisense DNA or RNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-615964/58.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ACH18176;
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(STAC/)
(DICK/)
(JONE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (DRMA/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genome
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The invention discloses a composition comprising two or more isolated rate or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that is differentially repressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more of more of more or more of pain and a pharmaceutical composition comprising the one or more of polypeptides or more of more or more of pain and a pharmaceutical composition comprising the one or more of more or                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New composition comprising two or more isolated polypeptides, useful for
for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at segdata.uspto.gov/sequence.html?DocID=20030073623
                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat; ds; gene; pain; neuronal tissue; gene therapy; Spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                       ö
                                                                                                                                                   Length 473;
                                                                                                   Sequence 473 BP; 142 A; 112 C; 114 G; 105 T; 0 U; 0 Other;
                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               preparing a medicament for treating pain in an animal
                                                                                                                                                   90.0%; Score 14.4; DB 9; 93.8%; Pred. No. 6.2e+02;
                                                                                                                                                                     93.8%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Costigan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rat gene AA892531, SEQ ID NO 5822.
                                                                                                                                                                                                                                                                                                                                                                                                                              ADE59926 standard; DNA; 504 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page; 1017pp; English.
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                                                                                                                                                                                                                                                                                                   383 ACCCCAAGGTTAACCC 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-AUG-2002; 2002WO-US025765.
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01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                    1 ACCCCAAGGITTACCC 16
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                                                                                                                                                                          Local Similarity 93.8
les 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADE59926;
                                                                                                                                                     Query Match
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The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector, comprising the nucleic acid sequence. Also comprising the vector, a method for identifying a nucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in the activity of one or more of the
                pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene therapy). The sequence presented is a rat DNA (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
modulates its activity is useful for preparing a medicament for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polynucleotides, a method for producing a pharmaceutical composition,
                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rat; ds; gene; pain; neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                                                                                                                                                                                                                               ٥;
                                                                                                                                                                                                                   , Match 90.0%; Score 14.4; DB 10; Length 504; Local Similarity 93.8%; Pred. No. 6.2e+02; tes 15; Conservative 0; Mismatches 1; Indels 0.
                                                                                                                                                                                  Seguence 504 BP; 78 A; 121 C; 210 G; 95 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Costigan M;
                                                                                                                                            ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat gene AA892531, SEQ ID NO 11406.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Befort K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                BP
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                                                                                                                                                                                                                                                                                                                                             406 ACCCCAAGGTCTACCC 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                                                                                                                       1 ACCCCAAGGTTTACCC 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                ADD45738 standard; DNA; 504
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus.
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GENBANK; AA892531
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADD45738;
                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                             Matches
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                                                                       compound that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
                                                                                                                                                                                       which is differentially expressed during pain. Note: The sequence data
for this patent did not form part of the printed specification, but was
obtained in electronic form directly from WIPO at
             activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polymucleotide or the compound th modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (Chung), chronic constriction injury (CLI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a rat DNA (shown in Table 2 of the specification) which encodes one of the polypeptides of the invention
for identifying a compound or small molecule that regulates the
                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel isolated nucleic acid molecule associated with cancerous state
                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                           90.0%; Score 14.4; DB 10; Length 504; 93.8%; Pred. No. 6.2e+02;
                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                       Sequence 504 BP; 78 A; 121 C; 210 G; 95 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human prostate expression marker cDNA 54259.
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                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABV54268 standard; cDNA; 509 BP
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; 2000US-0189862P.
; 2000US-0207454P.
; 2000US-0211314P.
; 2000US-0219007P.
                                                                                                                                                                                                                                                                                                                                                                                                                               406 ACCCCAAGGTCTACCC 391
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nes 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
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ABV54268/
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ACA43754 standard; DNA; 663 BP.

ACA43754/c RESULT 13

19-JUN-2003

ACA43754;

us-10-808-187a-2476.rng

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(e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (I) is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated polypeptide (I) associated with breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (S1). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention may be described as cytostatic. The antibody is useful for invention may be described as cytostatic. The antibody is useful for detection of (I) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (I) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN7881-ACN92934 represent nucleic acid markers associated with breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web
                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated polypeptide associated with breast cancer, useful for detecting presence of polypeptide in sample, as a marker for breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
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                                                                                                                                                        Length 509;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 site at segdata.uspto.gov/sequence.html?DocID=20030099974
                                                                                                                                                                                              1; Indels
                                                                                                                  Sequence 509 BP; 196 A; 77 C; 81 G; 152 T; 0 U; 3 Other;
                                                                                                                                                      90.0%; Score 14.4; DB 5; 93.8%; Pred. No. 6.2e+02;
                                                                                                                                                                                            0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Breast cancer related marker, seq id 8498.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Steinmann K;
                                                                                                                                                                                                                                                                                                                                                                     ACN87348 standard; DNA; 629 BP
                                                                                                                                                                                                                                                              289 ACCCCAAGGTTTTCCC 274
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                                                                                                                                                                                                                                1 ACCCCAAGGTTTACCC 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                            15; Conservative
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Best Local Similarity
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                                                                                                                                                                        Best Local Similarity
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                                                                                                                                                        Query Match
                                                                                                                                                                                            Matches
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The invention relates to an isolated nucleic acid comprising any one of
the 6213 antisense sequences given in the specification where expression
of the nucleic acid inhibits proliferation of a cell. Also included are:
(1) a vector comprising a promoter operably linked to the nucleic acid
encoding a polypeptide whose expression is inhibited by the antisense
to its fragment whose expression is inhibited by the antisense
compound acid; (4) an antibody capable of specifically binding
polypeptide or its fragment whose expression is inhibited by the
antisense nucleic acid; (4) an antibody capable of specifically binding
colliferation or the activity of a gene in operor required for
proliferation or the activity of a gene or peroliferation or the polypeptide, (5) producing the polypeptide; (6) inhibiting cellular
proliferation, (7) identifying a nactivity against a biological pathway
required for proliferation, or that inhibits cellular proliferation; (8)
identifying a gene required for cellular proliferation or the biological
compound's activity; (11) a culture comprising strains in which the gene
compound's activity; (11) a culture comprising strains in which the extent
compound's activity; (11) a culture comprising strains in which the extent
cownich each of the strains is present in a culture or collection of
strains; or (13) identifying the target of a compound that inhibits the
compound an organism. The antisense nucleic acids required
condiferation of an organism. The antisense nucleic acids required
for cellular proliferation to a solate candidate molecic acids required
for cellular proliferation of an organism. The antisense nucleic acids required
for cellular proliferation of an organism. The antisense nucleic acids required
for cellular proliferation of an organism. The antisense nucleic acids required
for cellular proliferation of an organism. The antisense molecules for rational
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zyskind JW;
Xu HH;
                                                                                                                                                                                  ds; prokaryotic essential gene; cell proliferation;
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Forsyth RA,
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Yamamoto R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 14; SEQ ID NO 31624; 1766pp; English.
                                                                                                                                 Prokaryotic essential gene #25411.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Malone C,
Carr GJ,
                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-2002; 2002WO-US009107.
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25-0CT-2001; 2001US-0342823P.
06-FEB-2002; 2002US-00072851.
06-MAR-2002; 2002US-03628991.
                                                                                                                                                                                                                                                                                                                                                                                                                                               21-MAR-2001; 2001US-00815242
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Trawick JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-029926/02.
P-PSDB; ABU39884.
                                                                                                                                                                                                                                                     Pseudomonas putida.
                                                                                                                                                                                                           drug design; gene
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                                                                                                                                                                                                                                                                                                                                                    03-OCT-2002
                                                                                                                                                                                  Antisense;
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Wall D,
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Gaps

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Indels

Length 629;

DB 11;

90.0%; Score 14.4; DB 11 93.8%; Pred. No. 6.3e+02;

Mismatches

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Conservative

611 ACCCCAAGGTTTTCCC 596

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1 ACCCCAAGGTTTACCC 16

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ADT45075;
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(SLAT/)
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(1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation or the activity of a gene in an operon required for proliferation, (7) identifying a compound that inhibits cellular proliferation; (8) identifying a gene rotivity against a biological pathway in which a proliferation or the biological pathway in which a proliferation or the biological pathway in which the test compound that inhibits proliferation of an companism acts; (9) manufacturing an antibiotic; (10) profiling a compound, a activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
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Xu HH;
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                                                                                                                 Length 663;
                                                          Sequence 663 BP; 140 A; 218 C; 193 G; 112 T; 0 U; 0 Other;
                                                                                                                                                                     Indels
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Forsyth RA,
                                                                                               90.0%; Score 14.4; DB 8;
ilarity 93.8%; Pred. No. 6.3e+02;
Conservative 0; Mismatches 1
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Yamamoto R,
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ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Prokaryotic essential gene #12147
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Carr GJ,
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25-OCT-2001; 2001US-034293P.
08-FEB-2002; 2002US-00072851
06-MAR-2002; 2002US-0362699P.
                                                                                                                                                                                                                                                                                    548 ACCTCAAGGTTTACCC 533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Campylobacter jejuni.
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Trawick JD,
                                                                                    Query Match
Best Local Similarity
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Wall D,
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to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Recombinant DNA construct; transformed plant; improved plant property; cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis; pathogen tolerance; pest tolerance; plant disease resistence; cell cycle pathway modification; plant growth regulator; homologous recombination; seed oil yield; protein yield; carbohydrate; nitrogen; phosphorus; photosynthesis; lignin; galactomannan; bacterial polymucleotide; gene; ss.
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Pred. No. 6.6e+02;
); Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published pct sequences
                                                                                                                                                                                                                                                                                                                                                                              format directly from WIPO at
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ses 15; Conservative
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(GOLD/) GOLDMAN B S.
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SLATER S C.
CHEN X.
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transformed plant having an improved property. The plant is a crop plant buth as maize or soybean. The method of producing a transformed plant having an improved property comprises transforming a plant with the recombinant DNA construct and growing the transformed plant, where the polynucleotide or polypeptide is useful for improving plant properties. The recombinant DNA construct is useful for improving plant properties. In improved plant properties, e.g. improved cold, heat or drought tolerance, to herbicides, extreme osmotic conditions, pathogens or peets, increased resistance to plant disease, better growth rate by modification of the cell cycle pathway with plant growth regulators, increased rate of homologous recombination, modified seed oil or protein yield and/or content, improved plant growth and development under at least one stress condition, improved plant growth and development under at least one stress condition, improved lignin production or improved galactomannan condition, improved lignin production or improved dalactomannan condition condition, improved lignin production or improved dalactomannan condition con lign $\overset{\circ}{\sim} \overset{\circ}{\sim} \overset{\circ}$

Sequence 1239 BP; 342 A; 278 C; 318 G; 301 T; 0 U; 0 Other;

Gaps ; 0 Query Match
90.0%; Score 14.4; DB 13; Length 1239;
Best Local Similarity 93.8%; Pred. No. 6.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0;

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Search completed: May 16, 2005, 01:09:40 Job time: 210.25 secs

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US-09-949-016-12384/c
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ORGANISM: Human
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LENGTH: 39154
FEATURE
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Sequence 12801, A
Sequence 14326, A
Sequence 14327, A
Sequence 16800, A
Sequence 7591, Ap
Sequence 22873, A
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Sequence 423, App
Sequence 1241, Ap
Sequence 81, Appl
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Sequence 158, App
Sequence 505, App
Sequence 429, App
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437.251 Million cell updates/sec
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// cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
// cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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Compugen Ltd.
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US-09-949-016-12801
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US-09-949-016-14327
US-09-949-016-16800
US-09-270-767-7591
US-09-270-767-7591
US-09-349-016-173609
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US-09-540-236-1241
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US-09-708-810-85
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Copyright (c) 1993 - 2005
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Listing first 45 summaries
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Sequence 12384, Application US/09949016

Patent No. 6812339

Patent No. 681239

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TURENT APPLICATION NUMBER: 60/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-00-03

PRIOR FILING DATE: 2000-00-03
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SEQUENCE 12801, Application US/09949016
SEQUENCE 12801, Application US/09949016
PAPLICANT: OF 12339
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT PELLIGN DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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                                                                             11, Appl
17255, A
16657, A
1, Appli
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15004, A
15694, A
15494, A
14957, A
11774, A
12147, A
14404, A
10528, A
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14036, A
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US-09-010-398-14
US-09-36-260-14
US-09-949-016-12576
US-09-949-016-12576
US-09-949-016-1755
US-09-949-016-1755
US-09-408-020-1
US-09-408-016-15604
US-09-949-016-15604
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US-09-949-016-15604
US-09-949-016-15604
US-09-949-016-11774
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US-09-949-016-12384
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Best Local Similarity 93.8
Matches 15; Conservative
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LOCATION: (1)...(39154)
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LENGTH: 39443
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Batent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILLE REFREENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

NUMBER OF SEQ ID NOS: 207012
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Fatent No. 6812339
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001307
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90.0%; Score 14.4; DB 4; Length 39154;
Best Local Similarity 93.8%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0;
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90.0%; Score 14.4; DB 4; Length 39443;
Best Local Similarity 93.8%; Pred. No. 2.9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0;
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-3
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PRASELSEQ FOR WINDOWS Version 4.0
SEQ ID NO 12801
LENGTH: 39154
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LOCATION: (1)...(39443)
OTHER INFORMATION: n = A,T,C or G
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i_CCATION: (1)...(39154)
i_CTHER INFORMATION: n = A,T,C or G
US-09-949-016-12801
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LENGTH: 39443
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307
TITLE OF INVENTION: WINDER: 10/109/949,016
CURRENT FILING DATE: 2000-10-14
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
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Pred. No. 4.6e+02;
0; Mismatches 0; Indels
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PILLING DATE: 2000-10-20
PRIOR FILLING DATE: 2000-10-20
PRIOR FILLING DATE: 2000-10-03
PRIOR FILLING DATE: 2000-10-03
PRIOR FILLING DATE: 2000-00-09
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASESEQ for Windows Version 4.0
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; LCCATION: (1)...(39443)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14327
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Best Local Similarity 100.
Matches 14; Conservative
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US-09-270-767-7591/c
                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Human
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US-09-949-016-16800
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; ORGANISM: Human
US-09-949-016-16800
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US-09-543-681A-423/C

Sequence 423, Application US/09543681A

Sequence 423, Application US/09543681A

Sequence 423, Application US/09543681A

Sequence 423, Application US/09543681A

Sequence 423, Application US/08509

GENERAL INFORMATION:

TITLE OF INVENTION:

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Pred. No. 7.1e+02;
0; Mismatches 1; Indels (
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APPLICANT: Burgess, Christopher C.
APPLICANT: Carroll III. Eddie
APPLICANT: Catrol, Theodore J.
APPLICANT: Catrol, Theodore J.
APPLICANT: Catrol, Theodore J.
APPLICANT: Derti, Adnan
APPLICANT: Derti, Adnan
APPLICANT: Lewis, Marcia E.
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Marcia E.
APPLIC
                                                                                                                                                                                                                                                                                                    Sequence 146, Application US/09328111
Patent No. 6262333
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; OTHER INFORMATION: n = A,T,C or G
US-09-328-111-146
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Endege, Wilson O.
APPLICANT: Steinmann, Kathleen E.
APPLICANT: Astle, Jon H.
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93.3%;
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11 Similarity 93.3%;
14; Conservative (
                                                                                        583 AACCCAAGGTTTACC 597
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US-09-543-681A-423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 93.3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
Matches 14; Conserv
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LENGTH: 735
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LENGTH: 624
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE REPERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PELICATION NUMBER: 60/241,756
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FESTERE CONTINGORDE SEG ID NOS: 207012
LENGTH: 601
LENGTH: 601
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APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REPERENCE: FILE REFERENCE: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: Parentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                Length 373;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
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83.8%; Score 13.4; DB 4;
Best Local Similarity 93.3%; Pred. No. 6.7e+02;
Matches 14; Conservative 0; Mismatches 1;
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Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-270-767-22873/c
; Sequence 22873, Application US/09270767
; Patent No. 6703491
                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Drosophila melanogaster
US-09-270-767-7591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Drosophila melanogaster
US-09-270-767-22873
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NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
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US-09-949-016-173609
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LENGTH: 373
                                                                                    SEQ ID NO 7591
LENGTH: 373
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APPLICANT: Kroger, Burkhard
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Hartwig
APPLICANT: Schroder, Gregor
TITLE OF INVENTION: CORNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
TITLE OF INVENTION: UNVOLVED IN HOMEOSTASIS AND ADAPTATION
FILE REFERENCE: BG1-128CP
CURRENT APPLICATION NUMBER: US/09/602,777A
FRIOR APPLICATION NUMBER: US 60/141031
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: DE 1993125.6
PRIOR FILING DATE: 1999-07-09
PRIOR FILING DATE: 1999-07-09
PRIOR APPLICATION NUMBER: DE 19932126.4
PRIOR FILING DATE: 1999-07-09
                                                                                                                                                                                                                 Sequence 65, Application US/09408020

Fatent No. 6632937
GENERAL INFORMATION:
APPLICANT: Samson, Ronald V.
APPLICANT: Relidman, Robert A.
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS FROM CENARCHAEUM SYMBIOSUM FILE REFERENCE: DCORP.002A
CURRENT APPLICATION NUMBER: US/09/408,020
CURRENT FILING DATE: 1999-09-29
FRIOR APPLICATION NUMBER: 60/102,294
PRIOR FILING DATE: 1998-09-29
NUMBER OF SEQ ID NOS: 123
SOUTHWARE: FREESEQ for Windows Version 3.0
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Best Local Similarity 93.3%; Pred. No. 7.5e+02; Matches 14; Conservative 0; Mismatches 1; Indels
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Pred. No. 7.6e+02;
0; Mismatches 1;
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; Sequence 409, Application US/09602777A
; Patent No. 6831165
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93.3%; Prer
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1268 ACCACAAGGITTACC 1254
                                                                                                       841 CCCCAAAGTTTACCC 855
                                                                 2 CCCCAAGGTTTACCC 16
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APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
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Best Local Similarity 93.3
Matches 14; Conservative
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; NAME/KEY: CDS
; LOCATION: (1)...(1512)
US-09-408-020-65
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US-09-408-020-65/c
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LENGTH: 1512
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Sequence 1241, Application US/09540236

Sequence 1241, Application US/09540236

GENERAL IN-6673910

GENERAL IN-673910

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR TITLE OF INVENTION: POSS DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 2709-200-001

CURRENT APPLICATION NUMBER: US/09/540,236

CURRENT APPLICATION NUMBER: US/09/540,236

MUMBER OF SEQ ID NOS: 3840
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TITLE OF INVENTION: No. 6783969el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 803
CURRENT APPLICATION NUMBER: US/09/799,451
CURRENT FILNG DATE: 2001-03-05
NUMBER OF SEQ ID NOS: 948
SOFTWARE: pt_FL_genes Version 2.0
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Patent No. 6783969
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Xue, Aidong J.
Zhao, Qing A.
Wang, Jian-Rui
Ma, Yunging
Yamazaki, Victoria
Chen, Rui-hong
                                                                 176 ccccaaggrrragcc 162
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APPLICANT: Zhou, Ping
APPLICANT: Goodrich, Ryle
APPLICANT: Asundi, Vinod
APPLICANT: Ren, Feiyan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 93.3
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: M.catarrhalis
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Drmanac, Rad
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; LOCATION: (63)..(1124)
US-09-799-451-81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-540-236-1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 81 TENGTH: 1270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
US-09-799-451-81
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APPLICANT:
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ORIGINAL SOURCE: INDIVIDUAL ISOLATE: Mouse alpha MHC promoter fragment
                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25-
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83.8%; Score 13.4; DB 2; 93.3%; Pred. No. 7.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                            APPLICATION NUMBER: US/08/365,486A
FILING DATE: 23-DEC-1994
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0860
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 1679 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Search completed: May 16, 2005, 06:11:47
Job time : 62.875 secs
  IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 93.3
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Webster, Keith A.
APPLICANT: Bishopric, Nanette H.
TITLE OF INVENTION: Tissue Specific Hypoxia Regulated
TITLE OF INVENTION: Therapeutic Constructs
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
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                                     PRIOR FILING DATE: 1999-07-14

PRIOR PELICATION NUMBER: DE 19912922.2

PRIOR APPLICATION NUMBER: DE 19912924.9.

PRIOR APPLICATION NUMBER: DE 19912924.9.

PRIOR PILING DATE: 1999-07-14

PRIOR FILING DATE: 1999-07-14

PRIOR PELING DATE: 1999-07-14

PRIOR PILING DATE: 1999-07-14

PRIOR PELING DATE: 1999-08-31

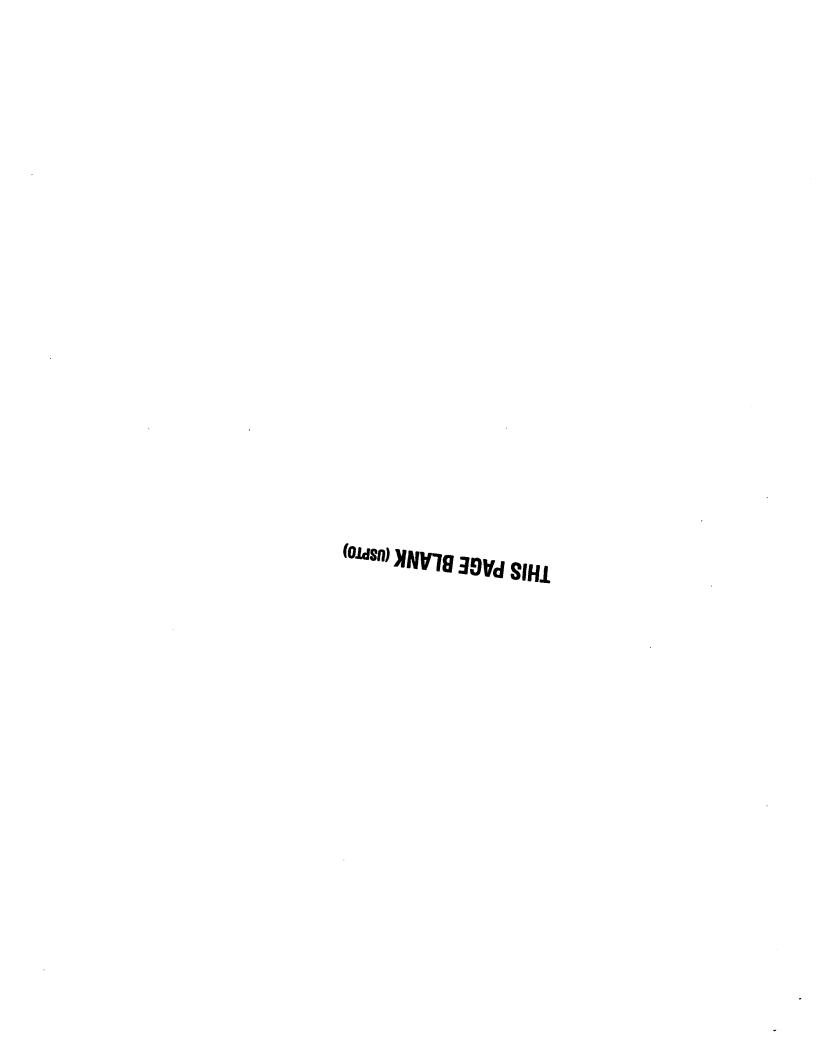
                       LING DATE: 1999-07-14
PLICATION NUMBER: DE 19932922.2
DE 19932920.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: DE 19941390.8
PRIOR FILING DATE: 1999-08-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19941391.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: DE 19942088.2
PRIOR FILING DATE: 1999-09-03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11, Application US/08365486A
Patent No. 5834306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1041 ACCCCAATGTTTACC 1055
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (101)..(1591)
; OTHER INFORMATION: RXN00641
US-09-602-777A-409
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Best Local Similarity 93.3%
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US-08-365-486A-11/c
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LENGTH: 1614
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Gaps

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Length 1679;



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May 16, 2005, 02:00:36 ; Search time 758.5 Seconds (without alignments) 129.102 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/USO6_NEW PUB.seq:*
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6: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
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12: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
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15: /cgn2_6/ptodata/1/pubpna/USO9_NEW PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5662332 seqs, 3060109652 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                           OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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16
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Query Match	Query Match Length DB	DB	ID	Description
-	16	100.0	16	19	:	Sequence 2476, Ap
7	16	100.0	1620	19	US-10-699-936-16	Sequence 16, Appl
٣	16	100.0	2304	19	US-10-699-936-7	Sequence 7, Appli
4	16	100.0		19	US-10-699-936-11	Sequence 11, Appl
S	16	100.0	~	19	US-10-889-447-3	." "
9	16	100.0		13	US-10-889-447-5	
7	16	100.0		19	US-10-889-447-6	Sequence 6, Appli
8	16	100.0		19	US-10-889-447-4	4
σ	16	100.0	29430	19	US-10-889-447-7	
10	16	100.0		18	US-10-839-729-15	15,
11	16	100.0		18	US-10-827-757-1	Sequence 1. Appli

Sequence 8, Appli Sequence 17, Appli Sequence 17, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 16, Appli Sequence 1108, Appli Sequence 1108, Appli Sequence 1108, Appli Sequence 10, Appli Sequence 10, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli	m	1012 1269 3093 798,
US-10-889-447-8 US-10-699-36-1 US-10-699-36-1 US-10-699-36-3 US-10-699-447-9 US-10-699-36-3 US-10-699-47-16 US-10-808-187-16 US-10-808-187-16 US-10-808-187-16 US-10-808-187-16 US-10-808-187-16 US-10-808-187-190 US-10-808-187-1905 US-10-808-187-1905 US-10-808-187-1905 US-10-899-447-10 US-10-626-879-67 US-10-626-879-67 US-10-626-879-67 US-10-629-3477-2 US-10-639-3447-2	US-10-424-599-40799 US-10-653-047-3616 US-10-424-599-67863 US-10-447-963-86252 US-09-974-300-3992 US-10-260-238-216 US-10-437-963-66704 US-10-444-696-89379	US-10-424-599-101240 US-10-425-115-126942 US-10-437-963-30933 US-10-950-009-798
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ALIGNMENTS

US-10 80B-187-2476

19-10 80B-187-2476

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Sequence 11, Application US/1069936

Publication No. US20050095582A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Taylor, Jill

APPLICANT: Scholl, David R.

APPLICANT: Wentworth, David B.

APPLICANT: Wentworth, David B.

APPLICANT: Wentworth, David B.

APPLICANT: World, Joseph D.

TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory

TITLE OF INVENTION: Syndrome Coronavirus

TITLE REFERENCE: DHI-07996

CURRENT APPLICATION NUMBER: US/10/699,936

CURRENT FILING DATE: 2003-11-03

NUMBER OF SEQ ID NOS: 87

SOFUR NO 11

TENTIFE PARTHER PATENTIAL VERSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                         Gaps
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US-10-889-447-3

Sequence 3, Application US/10889447

Publication No. US20050075307A1

GENERAL INFORMATION:

APPLICANT: Bennett, C. Frank

APPLICANT: Dain, Ravi

TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION

TITLE OF INVENTION WHERE: US/10/889,447

CURRENT APPLICATION NUMBER: 05/486,670

PRIOR APPLICAND NUMBER: 60/486,670

PRIOR FILING DATE: 2003-07-12

NUMBER OF SEQ ID NOS: 241

SOFTWARE: FastSEQ for Windows Version 4.0

LENGTH: 24774
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                       Length 2304;
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100.0%; Pred. No. 1e+02;
trive 0; Mismatches 0;
                       Query Match 100.0%; Score 16; DB 19; Best Local Similarity 100.0%; Pred. No. 98; Matches 16; Conservative 0; Mismatches 0;
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Pred. No. 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA ORGANISM: SARS coronavirus isolate BJ01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA; ORGANISM: SARS coronavirus Shanhgai LY
US-10-699-936-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: n is any nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; S
Best Local Similarity 100.0%; P
Matches 16; Conservative 0;
                                                                                                                                            880 ACCCCAAGGITTACCC 895
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Best Local Similarity 100.
Matches 16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Taylor, Jill
APPLICANT: Scholl, David R.
APPLICANT: Scholl, David R.
APPLICANT: Wentworth, David E.
APPLICANT: Wentworth, David E.
APPLICANT: Jollick, Joseph D.
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
TITLE OF INVENTION: Syndrome Coronavirus
FILE REFERENCE: DHI-07986
CURRENT APPLICATION NUMBER: US/10/699,936
CURRENT FILING DATE: 2003-11-03
NUMBER OF SEQ ID NOS: 87
SOFTMARE: PatentIn version 3.2
SEQ ID NO 16
LENGTH: 1620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Gillim-Ross, Laura
APPLICANT: Gillim-Ross, Laura
APPLICANT: Taylor, Jill
APPLICANT: Scholl, David R.
APPLICANT: Scholl, David R.
APPLICANT: Wentworth, David E.
APPLICANT: Joilick, Joseph D.
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
TITLE OF INVENTION: Syndrome Coronavirus
FILE REFERENCE: DHI-07986
CURRENT APPLICATION NUMBER: US/10/699,936
CURRENT FILING DATE: 2003-11-03
NUMBER OF SEQ ID NOS: 87
SOFTWARR: Patentin version 3.2
SEQ ID NO 7
LENGTH: 2304
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Pred. No. 97;
                                                                                                                                       FEATURE:
, OTHER INFORMATION: Description of Artificial Sequence: Probe US-10-808-187-2476
                                                                                                                                                                                                                                    19; Length 16;
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Publication No. US20050095582A1
GENERAL INFORMATION:
APPLICANT: Gillim-Ross, Laura
APPLICANT: Taylor, Jill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 7, Application US/10699936 Publication No. US20050095582A1 GENERAL INFORMATION:
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Best Local Similarity 100.0%; P. Matches 16; Conservative 0;
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; ORGANISM: SARS-COV Shanghai LY
US-10-699-936-7
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                                                                                          TYPE: DNA
ORGANISM: Artificial Sequence
NUMBER OF SEQ ID NOS: 2476
SOFTWARE: PatentIn ver. 3.2
SEQ ID NO 2476
LENGTH: 16
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ORGANISM: SARS-COV ZJ-HZ01
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US-10-699-936-16
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SEQ ID NO 5 LENGTH: 28920

US-10-889-447-5

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LOCATION

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Sequence 4, Application US/10889447
Publication No. US20050075307A1
GENERAL INFORMATION:
APPLICANT: Dain, Ravi
TILE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
FILE REFRENCE: RTS-0685US
CURRENT TILING DATE: 2004-07-12
PRIOR APPLICATION NUMBER: US/10/889,447
PRIOR APPLICATION NUMBER: 05/486,670
PRIOR FILING DATE: 2003-07-12
NUMBER OF SEQ ID NOS: 241
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 4
LENGTH: 29291
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TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
TITLE REPERENCE: RTS-0685US
CURRENT APPLICATION NUMBER: US/10/889,447
CURRENT FILING DATE: 2004-07-12
PRIOR PAPLICATION NUMBER: 60/486,670
PRIOR FILING DATE: 2003-07-12
NUMBER OF SEQ ID NOS: 241
SOFTWARE: FRASEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 29430
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-hag 0; Indels
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; Publication No. US20050002953A1
; GENERAL INFORMATION:
APPLICANT: Jons Herold
; TITLE OF INVENTION: SARS-CORONAVIRUS VIRUS-LIKE PARTICLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 16; DB 19; 100.0%; Pred. No. 1e+02;
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ORGANISM: SARS coronavirus isolate GZ01
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US-10-889-447-4
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COTHER INFORMATION: n is any nucleotide
US-10-889-447-7
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Best Local Similarity 100.0
Matches 16; Conservative
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Matches 16; Conservative
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NAME/KEY: misc_feature
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US-10-839-729-15
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100.0%; Pred. No. 1e+02;
tive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                     APPLICANT: Bennett, C. Frank
APPLICANT: Bennett, C. Frank
TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
FILE REFERENCE: TRS-0685US
CURRENT APPLICATION NUMBER: US/10/889,447
CURRENT FILING DATE: 2004-07-12
PRIOR APPLICATION NUMBER: 60/486,670
PRIOR PILING DATE: 2003-07-12
NUMBER OF SEQ ID NOS: 241
SOFTWARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
FILE REFERENCE: RTS-0685US
CURRENT APPLICATION NUMBER: US/10/889,447
PRIOR APPLICATION NUMBER: 60/486,670
PRIOR APPLICATION NUMBER: 60/486,670
PRIOR FILING DATE: 2003-07-12
NUMBER OF SEQ ID NOS: 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: SARS coronavirus isolate BJ03
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; OTHER INFORMATION: n is any nucleotide
US-10-889-447-6
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                                                                                          US-10-889-447-5; Sequence 5, Application US/10889447; Publication No. US20050075307A1; GENERAL INFORMATION:
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Publication No. US20050075307A1
GENERAL INFORMATION:
APPLICANT: Bennett, C. Frank
    23358 ACCCCAAGGTTTACCC 23373
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Best Local Similarity 100.0
Matches 16; Conservative
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US-10-889-447-6

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SEQ ID NO 6 LENGTH: 28920

TYPE: DNA

RESULT 8 US-10-889-447-4

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us-10-808-187a-2476.rnpb

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APPLICANT: Gillim-Ross, Laura
APPLICANT: Taylor, Jill
APPLICANT: Wentworth, David R.
APPLICANT: Gollick, Joseph D.
TITLE OF INVENTION: Compositions and Methods for Detecting Severe Acute Respiratory
TITLE OF INVENTION: Syndrome Coronavirus
FILE REFERENCE: DHI-07986
CURRENT APPLICATION NUMBER: US/10/699,936
CURRENT FILING DATE: 2003-11-03
NUMBER OF SEQ ID NOS: 87
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                                         100.0%; Score 16; DB 19; Length 29727; 100.0%; Pred. No. 10+02; ive 0; Mismatches 0; Indels 0;
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Sequence 17, Application US/10839729

Publication Wo. US20050002953A1

GENERAL INFORMATION:

APPLICANT: Jens Herold

ITLE OF INVENTION: AND METHODS OF USE

ITLE OF INVENTION: AND METHODS OF USE

CURRENT APPLICATION NUMBER: US/10/839,729

CURRENT FILING DATE: 2004-05-04

PRIOR PILING DATE: 2003-05-06
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100.0%; Score 16; DB 19; Length 2:
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels
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100.0%; Pred. No. 1e+02;
ive 0; Mismatches 0; Indels
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                          ; Sequence 1, Application US/10699936; Publication No. US20050095582A1; GENERAL INFORMATION:
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ORGANISM: SARS Coronavirus
US-10-839-729-17
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Best Local Similarity 100.º
Matches 16; Conservative
                                       Query Match
Best Local Similarity 100."
Matches 16; Conservative
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LENGTH: 29727
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LENGTH: 29736
    US-10-889-447-8
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Sequence 1, Application US/10827757

Sublication No. US2005004071A1

GENERAL INFORMATION:
APPLICANT: Comper, Wayne
TITLE OF INVENTION: Charged Polysaccharides Resistant To Lysosomal Degradation During
TITLE OF INVENTION: Kidney Filtration And Renal Passage And Their Use To Treat Or
TITLE OF INVENTION: Whomer: US/10/827,757

CURRENT APPLICATION NUMBER: US/10/827,757

CURRENT FILING DATE: 2004-04-20

PRIOR APPLICATION NUMBER: 60/464,294

PRIOR FILING DATE: 2003-04-21

NUMBER OF SEQ ID NOS: 1

SOPTWARE: PatentIn version 3.2
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Publication No. US20050075307A1
GENERAL INFORMATION:
APPLICANT: Bennet', C. Frank
APPLICANT: Jain, Ravi
TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION
FILE REPERENCE: RTS-0665US
CURRENT APPLICATION NUMBER: US/10/889,447
PRIOR APPLICATION NUMBER: 60/486,670
PRIOR PILING DATE: 2003-07-12
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ORGANISM: SARS-related coronavirus (Urbani strain)
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TITLE OF INVENTION: AND METHODS OF USE
FILE REFERENCE: BIODANK. 013A
CURRENT APPLICATION NUMBER: US/10/839,729
CURRENT FILING DATE: 2004-05-04
PRIOR APPLICATION NUMBER: 60/468703
PRIOR FILING DATE: 2003-05-06
NUMBER OF SEQ ID NOS: 49
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15
LENGTH: 29727
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 29727
TYPE: DNA
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Best Local Similarity 100.0
Matches 16; Conservative
                                                                                                                                                                                                                           TYPE: DNA ORGANISM: SARS Coronavirus
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LENGTH: 29727
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US-10-827-757-1
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RESULT 15

US-10-889-447-9

i Sequence 9, Application US/10889447

i Publication No. US20050075307A1

i GENERAL INFORMATION:
    APPLICANT: Bennett, C. Frank

i APPLICANT: Bennett, C. Frank

i APPLICANT: Bennett, C. Frank

i TITLE OF INVENTION: MODULATION OF AMINOPEPTIDASE N EXPRESSION

TITLE REFERENCE: REJ. 6085US

CURRENT APPLICATION NUMBER: US/10/889,447

CURRENT APPLICATION NUMBER: 60/486,670

PRIOR APPLICATION NUMBER: 60/486,670

PRIOR PELLING DATE: 2003-07-12

NUMBER OF SEQ ID NOS: 241

SOFTWARE: FastSEQ for Windows Version 4.0

SOFTWARE: FastSEQ for Windows Version 4.0

CORGANISM: SARS coronavirus CUHK-W1

US-10-889-447-9

Query Match

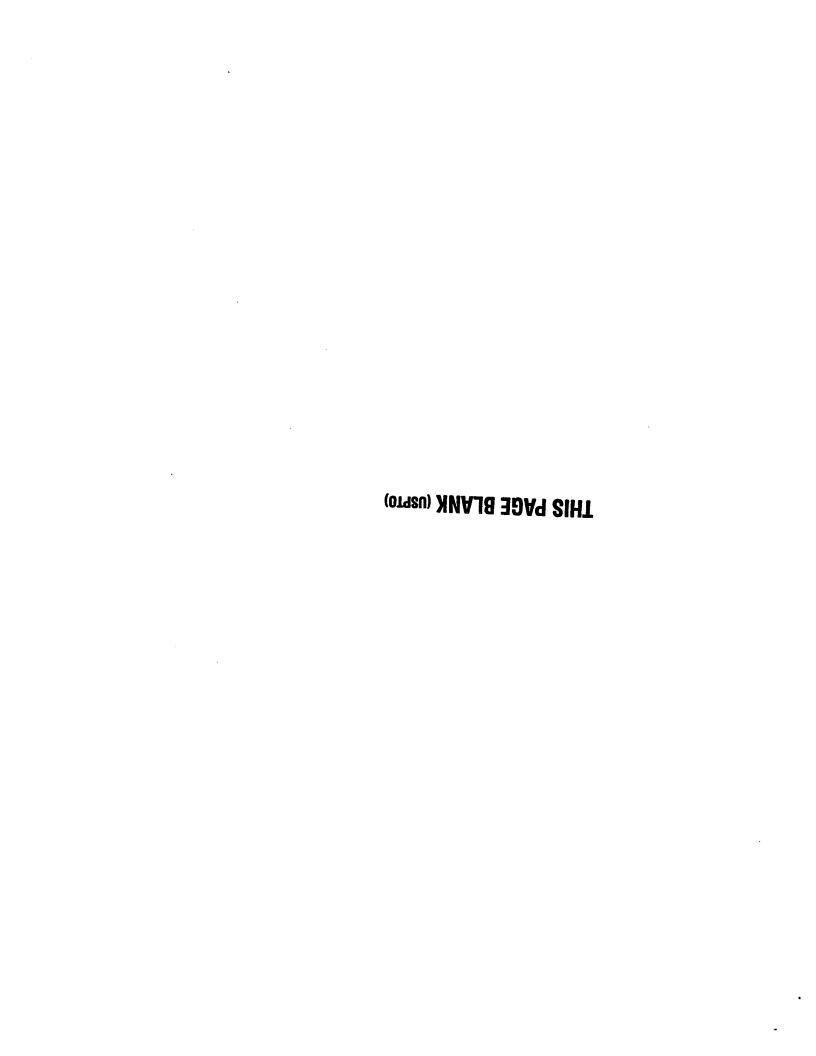
DOUGNIATION: Pred. No. 16+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps

ON 28230 ACCCCAAGGTTTACCC 16

DD 28230 ACCCCAAGGTTTACCC 28245
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Search completed: May 16, 2005, 14:33:52 Job time : 760.5 secs



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Makaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, eudicotyledons, core eudicots;
rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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BP653652 RAFL19 Arabidopsis thaliana cDNA clone RAFL19-14-M03 3',
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BJ535173
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/db_xref="taxon:3702"
/clone="RRF119-14-M03"
/tissue_type="mixture of silique and flower"
/lab host="DH108"
/clone_lib="RAF119"
/note="Site_1: BamH1; Site_2: SalI; Subtraction
                                             BJ005175 EBJ00302 EBJ013062 EBJ013062 EBJ013065 EBJ012095 EBJ02217 EBJ02217 EBJ012751 EBJ017517 EBJ01751 EBJ01
BJ532637 B
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Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Fal: 81-298-36-4359
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Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 16; Conservative 0; Mismatches 0;
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                GenCore version
Copyright (c) 1993 - 2005
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Gapop 10.0 , Gapext 1.0
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Genoscope.
Direct Submission
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Submitted (15-FEB-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Location/Qualifiers
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Submitted (25-FEB-2004) Genoscope - Centre National de Sequencage :
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Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
/note="Vector: pBeloBAC11 ; Site 1: HindIII ; Site 2: HindIII ; Cook, D.R. and Kim, D.J~Genoscope sequence ID mth2-188J7FM1"
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Pred. No. 4.1e+02;
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/organism="Medicago truncatula"
/mol type="genomic DNA"
/culTivar="Jemalong A17"
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TITLE
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Submitted (10-JUN-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (B-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr | Location/Qualifiers
                                                                                                                                       CR488879 514 bp DNA linear GSS 11-JUN-2004
Medicago truncatula BAC ends cultivar Jemalong A17 of Medicago
truncatula, genomic survey sequence.
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Direct Submission
Submitted (10-JUN-2004) Genoscope - Centre National de Sequencage : Submitted (10-JUN-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr - Web : www.genoscope.cns.fr - Web : www.genoscope.cns.fr - Location/Qualifiers
                                                                                                                                                                                                                                                                                  Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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/coln type="genomic DNA"
/db xref="taxon:3880"
/clone lib="MTH2"
/note="Vector: pBelobAC11; Site 1: HindIII; Site_2:
HindIII; Cook, D.R. and Kim, D.J~Genoscope sequence ID
mth2-15946FM1"
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/mol type="genomic DNA"
/cultivar="Joenalong A17"
/db xref="taxon:380"
/clone_lib="WTH2"
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        1 ACCCCAAGGITTACCC
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Length 759;

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100.0%; Score 16; DB 6; I 100.0%; Pred. No. 4.4e+02; Live 0; Mismatches 0;
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                                                                1 ACCCCAAGGTTTACCC 16
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                                 Conservative
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Best Local Similarity
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AGENCOURT 13645873 NIH MGC_184 Homo sapiens cDNA clone
IMAGES30329411 5', mRNA sequence.
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Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
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                                                                                                                                    /note="Vector: pIndigoBAC ; Site_I: EcoRI ; Site_2: EcoRI ; Debelle F. and Chalhoub B.~Genoscope sequence ID : mte1-82N15FM1"
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM141 row: j column: 12
High quality sequence stop: 468.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                        /organism="Medicago truncatula"
/mol type="genomic DNA"
/cultivat="Vemalong A17"
/db xref="taxon:380"
/clone_lib="MTE1"
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              - Web : www.genoscope.cns.fr)
Location/Qualifiers
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/lab host="DH10B"
/clone lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
ECORI; Site_2: ECORI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of ECORI and ECORI Methylase. Size
gelected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies). "
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Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de
Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Seq primer: T7
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Fel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse BAC End Sequences from Library RPCI-23 Unpublished (1999)
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-209L13"
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
Fhis sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.infobiogen.fr).
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Location/Qualifiers
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/cultivar="recital"
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G118.110J07P010720 G118 Triticum aestivum cDNA clone G118110J07,
mRNA seguence.
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Triticum aestivum
Triticum aestivum
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta; Liliopsida, Poales, Poaceae;
Pooideae, Triticeae, Triticum.
                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1017)
NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2951 row: j column: 21
High quality sequence stop: 579.
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BU931691 10472385 NIH_MGC_109 mRNA linear EST
AGENCOURT 10472385 NIH_MGC_109 Homo sapiens cDNA clone
IMAGE:6671925 5', mRNA sequence.
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Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 16; Conservative 0; Mismatches 0;
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/db_xref="taxon:9606"
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Homo sapiens
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wdklc.pk024.j5 wdklc Triticum aestivum cDNA clone wdklc.pk024.j5 s'cA706577
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Triticum aestivum
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
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/tissue type="kernel"
/clone=lwdklc.pk024.js"
/note="Vector: pBluescript SK+; Wheat (Triticum aestivum
L.) developing kernel, 3 days after anthesis."
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DuPont Wheat cDNA Sequence
Unpublished (2002)
Contact: Scott V. Tingey
Crop Genetics
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1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA
Tel: 302-631-2602
Fax: 302-631-2607
Email: Scott.V.Tingey@USA.dupont.com
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                                                                                                                /tissue type="grain (118 degrees per day after pollination)" /clone_lib="G118"
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                                                                                                                                                                                                                                      93.8%; Score 15; DB 6; Length 391; 100.0%; Pred. No. 1.4e+03;
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/organism="Triticum aestivum"
                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                    /db_xref="taxon:4565"
/clone="G118110J07"
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us-10-808-187a-2476.rst

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/lab_host="E. col SOLA"
/lab_host="E. col SOLA"
/lab_host="Wector: Lambda ZAP II, excised phagemid; Site_1:
/note="Vector: Lambda ZAP II, excised phagemi
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Brassica.
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Contact: Genoplante
Genoplante
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Location/Qualifiers
                                                                                                                      Tel. 5105595773
Fax: 5105595818
Fax: 5105595818
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
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Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
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/cultivar="samourai (restored line)"
                                                                                                                                                                                                                                                                                                                                                                                  /organism="Triticum aestivum"
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/tissue_type="anthers"
/clone_lib="RFO2"
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 425)
Seki, M. Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T.,
Sakajima, M., Enju, A., Akiyama, K., Oono, Y., Muramateu, M.,
Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y.,
Arakawa, T., Shibata, K., Shinagawa, A. and Shinozaki, K.
Functional annotation of a full-length Arabidopsis cDNA collection
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1 (bases 1 to 480)
Altenbach, S., Anderson, O.D., Chao, S., Galili, G., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and Tong, J.C.
The structure and function of the expressed portion of the wheat genomes - Endosperm cDNA library
Unpublished (2000)
                                                                                                                                                                                                                                                                            Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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/note="Site_1: BamHI; Site_2: SalI; Subtraction Library.
The sequence was obtained from samples subjected to
various stress and plant hormones-treated"
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reversed clone; Please visit our web site
(http://pfgweb.gsc.riken.go.jp/) for further details.
Location/Qualifiers
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Plant Functional Genomics Research Group
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/clone="RAFL21-02-A07"
/lab_host="DH10B"
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Triticum aestivum
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RESULT 11
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BJ538102 MF01SSB cDNA Oryzias latipes cDNA clone MF01SSB008H23 3',
mRNA sequence.
BJ538102
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Seki, M., Narusaka, M., Kamiya, A., Ishida, J., Satou, M., Sakurai, T.,
Nakajima, M., Enju, A., Akiyama, K., Oono, Y., Muramateu, M.,
Hayashizaki, Y., Kawai, J., Carninci, P., Itoh, M., Ishii, Y.,
Hayashizaki, Y., Shibaqawa, A., and Shinozaki, K.
Functional annotation of a full-length Arabidopsis cDNA collection
Science 296 (5565), 141-145 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Oryzias latipes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
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93.8%; Score 15; DB 6; Length 496; 100.0%; Pred. No. 1.5e+03; ive 0; Mismatches 0; Indels
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Plant Functional Genomics Research Group
RIKEN Genomic Sciences Center
3.1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9060
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
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/organism="Arabidopsis thaliana"
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Best Local Similarity 100.
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Query Match 93.8
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                                             Kohara, Y., Shin-i, T., Kimura, T., Narita, T., Jindo, T. and Takeda, H. Medaka EST Project in Takeda's lab Medaka EST Project in Takeda's lab Unpublished (2001)
Contact: Tadasu Shin-i
Contact: Tadasu Shin-i
Contact: For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
Exai: 15hihi@genes.nig.ac.jp.
Location/Qualifiers
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Acanthomorpha; Acanthopterygii; Percomorpha; Atherinomorpha;
Beloniformes; Adrianichthyidae; Oryzinae; Oryzias.
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/fissue_type="whole embryo"
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100.0%; Pred. No. 1.5e+03;
ive 0; Mismatches 0;
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/strain="Hd-rR"
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Best Local Similarity 100.
Matches 15; Conservative
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Search completed: May 16, 2005, 06:03:51 Job time : 1814 secs